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181 GGAGGAGTGGAACGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCGGTC

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Oy 1321 AACGTTCATCTCCACACCTACTGTATATGGCATGCTCGGC 13	RESULT 2 AX490719 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	ORGANISM ORGANISM REFERENCE AUTHORS	Chan, R.  TITLE Phosphatase stress-related proteins and method JOURNAL Patent: WO 0246442-A 8 13-JUN-2002; BASF Plant Science GmbH (DE) FEATURES Location/Qualifiers 1. 1365 //renanisme.Physcomitrella patens"	/mol_type="unassigned DNA" /db_xref="taxon:3218" )	Query Match 100.0%; Score 1365; DB 6; Length Best Local Similarity 100.0%; Pred. No. 0; Matches 1365; Conservative 0; Mismatches 0; Indels	OY 1 GGCGTTAACGCGCGGAGAGAGAGAGATCGGTTAGGGTTTGGTGCCAGGGG	Db 61 GGTTGGGACAATGCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC	QY         121 CAAGCCGTTGTCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGGA           DD         121 CAAGCCGTTGTCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGGA	DD 181 GGAGGAGTGGAACGTGCAGCCGTGAAGTGTCCTGTCAGGTTGCGGTG.	20 241 CCAGITTCATGATCTCATCGAGCTTTTCCGCATAGGAGGAGGGCGCCG. 20 Db 241 CCAGITTCATGATCTCATCGAGCTTTTCCGCATAGGAGGAGGAGGCGCCCG.	301 CTTGTTCATGGGCGACTATGTGGATCGTGGATATTATTCTCTCGAGACTG	10 Qy 361 AGTGGCCCTGAAGGTGCGGTATAGGGATAGGATCACAATCTTGCGAGGA.	00 421 CAGGCAGATTACGCAAGTATATGGTTTCTATGATGATGCCTGCGGAAGT.	50 QY 481 GAATGTTTGGAAGTACTTCACGGATCTGTCGACTACTGACAG	20 S41 GCACGAGATTTTTTGTCTTCATGGTGTCTGTCTCCATCGCTCGACACATT
181 GCAGGAGTGGAACGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCGGTGACATCCATGG 240 241 CCAGTTTCATGATCTCATCGAGCTTTTCCGCATAGGAGGCAAGGCGCCCGACACGAACTA 300 [		421 CAGGCAGATACGCAAGTATATGGTTTCTATGATGAAGCCTGCGGAAGTATGGAAATGC 480		601 CCGAGCCCTAGATCGTATTCAAGAAGTGCCGCACGAGGGCCCGATGTGTGATCTACTCTG 660	661 GTCTGATCCAGATGATGTGGATGGGGGATTTCACCACGAGGTGCCGGTTATACTTT 720	721 TGGTCAAGATATTGCAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGCACGTGC 780	781 TCACCAGCTTGTGATGGAAGGATACAATTGGTGCCAGGATAAAATGTTGTCACAGTTTT 840 	841 CAGIGCCCCCAAITACIGITACCGCTGIGGGAACAIGGCCGCCAIAAIGGAGAIGAGAI	901 AACAATGAATCGGTCTTTTCTTCAGTTCGAACCAGCACCGCGGCAAAGTGAACCAGAATGT 960 	961 GACGCGGAAGACTCCTGATTACTTTCTGTAAACATGGCCTATACATGGTACCTTTTACTT 1020 	1021 ACTGAATTGTTCTGTATAGTCACCTTCCATGGAAGCAGTTTGCCCCTGAATGAA	1081 CCCTCATGATCTAGTATGAAGTTATCTTTTGAAGTGTTTGTT	1141 CTTGCTCCTCTGTTCATTCATAAAGTTGCCTTCAGAACAACTGAGAATGTTGTGAATGTAA 1200	1201 CTGCGACAAGAGGAGCAGTGTCAATGGTTGCAAGGGTTATAGTGATTAGGGAAAGAAGGT 1260 	1261 AGCACATGTTACTTCAAATCGATCAGAGACTTCTATGGAAAAGATGACGATGGTGGAAAC 1320

3T 180

3G 240 3G 240 7A 300

3C 480 3C 480 3A 540 3A 540 7T 600 7T 600

	GC 780 	GA 900 GA 900 GT 960 GT 960		TA 1140 	
CCGAGCCCTAGATCGTATTCAAGAAGTGCCGCACGAGGGCCCCGATGTGTGTTCTTCTGCGGGGCCCCGATGTGTTGTTTCTAGAGTGCCGCACGAGGGCCCCGATGTGTTGTTTTCAAGAAGTGCCGCACGAGGGCCCGATGTGTTGTTTTTTTT	PGSTCAAGATATTGCAAGGCAGTTCATACCAATGGTCTAAGTTTGGTTGCACGTGC TGGTCAAGATATTGCAGGCGGTTCAATCATACCAATGGTCTAAGGTTGGGTTGCACGTGC TGGTCAAGATATTGCAGGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGCACGTGC TCACCAGCTTGTGATGGAAGGATACCAATTGGTGCCAGGATAAAAATGTTGTCACAGTTTT TCACCAGCTTGTGATGGAAGGATACAATTGGTGCCAGGATAAAAATGTTGTCACAGTTTT TCACCAGCTTGTGATGGAAGAATACAATTGGTGCCAGGATAAAAATGTTGTCACAGTTTT	CAGTGCCCCCAATTACTGTTACCGCTGTGGGAACATGGCCGCCATAATGGAGATAGAT	GACGCGGAAGACTCCTGATTACTTTCTGTAAACATGGCCTATACATGGTACCTTTTACTT  [	CCCTCATGATCTAGTAGTATGAAGTTATCTTTGAAGTGTTTGTT	AGCACATGTTACTTCAAATCGATCAGAGACTTCTATGGAAAGATGACGATGGTGGÀAAC AGCAATGTTACTTCAAATCGATCAGAGACTTCTATGGAAAGATGACGATGGTGGÀAAC AACGTTCATCTCCACACATCAGAGACTTCTATGGAAAGATGACGATGGTGGAAAAC AACGTTCATCTCCACACCTACTGATGGCATGCTCGAGCTCGC 1365 AACGTTCATCTCCCACCTACTGTATATGGCATGCTCGAGCTCGC 1365 AACGTTCATCTCCCACCTACTGTATATGGCATGCTCGAGCTCGC 1365
· -	TCACCAGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	CAGTGCCCCCATI	GACGCGGAAGACT	CCCTCATGATCTA	AGCACATGTTACT
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6 6 6 6 6	2 2 2 2	8 6 6 6	8 8 8 8	6 6 6 6 6	8686

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1380 bp mRNA linear PLN 05-MAY-2004
(PP2Ac1) mRNA, complete cds.
AY325817
AY325817.1 GI:34398260
RESULT 3
AY325817
LOCUS
DEFINITION
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Lycopersicon esculentum (Solanum lycopersicum) ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Lycopersicon esculentum (Streptophyta; Embryophyta; Exacheophyta; Exacyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 1380)
He,X., Anderson,J.C., Pozo Od,O., Gu,Y.O., Tang,X. and Martin,G.B. Silencing of subfamily I of protein phosphatase 2A catalytic subunits results in activation of plant defense responses and localized cell death REFERENCE AUTHORS TITLE

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EEWNVQP LLVALKV ALIESQI GAGYTFG AAILEIS 120 319 180 379 240 439 300 499 360 559 420 619 480 619 540 739 600 5=5 1=1 FH-F g=g¥=¥ AG-AG ႘ႍ႘ 8=8 A-A-T / note:
// foodon start=1
/ product="protein phosphatase 2A catalytic
/ protein id="Ad06725.1"
/ bxee="d1:34398261"
/ translation="MPSHADVDRQIEGLMECKPLSEAEVKTLC
VKCPVTVGDIHGGPYDLIELPRIGGNLITNYLEMGDYVDRG
RYRDRITLLEGNHESRQITOVYGFYDECLRKYGNANVHKYFTI
FCLHGGLSPSLDTLDNIRALDRIQEVPHEGPMCDLLWSDPDDF
QDIAQQFWHTNGLSPSLISRAHQLVMEGFNWCQDKNVTVFSAPN
ENMEDNFLOFDPAPRQIEPDTTRKTPDYFL"
1191. 11380 Leases 1 to 1380)

He,X., Anderson,J.C., del Pozo,O., Gu,Y.-Q., Tang,X. Martin,G.B.

Direct Submission

Submitted (18-JUN-2003) Boyce Thompson Institute, Cc University, Tower Road, Ithaca, NY 14853, USA

Location/Qualifiers DB 15; Length 1 440 ACAGTTTTACGATCTGATTGAGCTTTTTCGAATCGGCGGCAACGTCCTGA 500 TCTCTTCATGGGAGATTATGTTGACCGTGGATACTATTCTGTCGAGACTC GGTTGGGACAATGCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC 260 GTTTGAAAAATGCCGTCGCACGCGATGTAGATCGGCAGATCGAGCAAT CAAGCCGTTGTCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGGA 320 caagccerrarcegagecegagereaagacerrerereagacaagee GGAGGAGTGGAACGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCCGGTG 380 geaggaargeaargrecaaccegreaargrecegreacgcrere 241 CCAGITICAIGAICICAICGAGCITITICCGCAIAGGAGGCAAGGCGCCCG 361 AGTGGCCCTGAAGGTGCGGTATAGGGATAGGATCACAATCTTGCGAGGGA gerrecrrreaaegrrecrraraeagaraeaareaearrerraegegaa GAATGTTTGGAAGTACTTCACGGATCTGTTCGACTACCTGCCTCTGACAG GCACGAGATTTTTGTCTTCATGGTGGTCTGTCTCCATCGCTCGACAT GAGTCAGATATTCTGTTTGCATGGAGGACTCTCACCATCCCTTGATACAC 301 CTTGTTCATGGGCGACTATGTGGATCGTGGATATTATTCTGTCGAGACTC CAGGCAGATTACGCAAGTATATGGTTTCTATGATGAATGCCTGCGGAAGT 42.9%; Score 585.8; DB 15; Length 76.7%; Pred. No. 3.8e-165; tive 0; Mismatches 217; Indels 1. .1380, General of contents note="LePP2Ac1" 270. .1190 /gene="PP2Ac1" /gene="PP2Ac1" Query Match
Best Local Similarity 76.7%
...nhe 716; Conservative 15125764 121 181 421 481 680 541 61 560 620 S'UTR 3'UTR REFERENCE AUTHORS TITLE JOURNAL gene PUBMED CDS FEATURES ORIGIN a ద g g 원 장 g ò ઠ ò ઠે ò à g ò a ઠે

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A 71 A 169 34 169 3T 131 G 229

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rc 911 || |C 1009

2A 851 | 1A 949

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TT 487 | TC 672

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CC 847 CT 1032

AG 787 || AG 972

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AT 667 || |AT 852

AA 727 | AG 912 TG 907 || TG 1092

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Yoshimura, A., Miura, J.

Камашата, М.,

Ishibiki,J.,

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Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakwa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayacsu,N., Imocani,K., Ishihi,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
1shikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 205-802, Japan (E-mail:sKikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fas.81-29-838-7007, Fas.81-29-838-7007, Fas.81-29-838-7007, Fas.81-29-808-7007, Fas.81-20-808 Full-length cDNA clones from japonica
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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DB 15;
                                 0; Mismatches 222;
 Score 582.8; DB 1
Pred. No. 3.2e-164
42.7%;
                Best Local Similarity 76.3
Matches 716; Conservative
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Mizuno,K., Narikawa,R., Suzuki,Y., Sugiyama,A., Mateubara, Yoshimura,A., Mateubara, Genome Exploration Resea and Genome Science Labox Akimura,T., Arakawa,T., Hara,A., Hashizume,W., Hiraoka,T., Hori,F., Iid Itoh,M., Kagawa,I., Kana Kishikawa Hirozanc,T., Koya,S., Kurihara,C., Ma Nakamura,M., Nishi,K., Nota,W., Yakamura,M., Vishi,K., Nota,W., Yakamura,M., Nishi,K., Nota,W., Sakai, Sagabe,Y., Taqami,M., Tarakaku-Akahira,S., Tanak Yakunishi,A. and Hayashi, FEATURES Location/Qualif Source /mol_type="marka"	/culturar="Nupp"/db_tref="taxon"/db_tref="taxo	115	, 2 175 132 235	Oy 192 ACGTGCAGCCGTGAAGTGTCC	415 372 475 432	0y
		japonica rice AL Science 301 (5631), 376-379 (2003) ED 12869764 CE 2 (bases 1 to 1376)	RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramcto, K., Hiracka, T., Hotte, I., Iida, J., Iida, Y., Ikeda, R., Immura, K., Immura, K., Immura, K., Kanajawa, S., Katoh, H., Kawagashira, N., Kawanata, M., Kayama, I., Kibuch, S., Katoh, H., Kawagashira, N., Kawanata, M., Kayama, I., Kayamata, M., Kayama, J., Kayamata, M.,	Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Muratami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Otca, Y., Otomo, Y., Ryu, R., Saito, K., Sakai, C., Sakai, K., Sakai, M., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,	Suglyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Suglyama, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tagami, T., Tsunoda, Y., Takaku-Akahira, S., Tanaka, T., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, O., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.  Direct Submission  Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Isukuba, Ibaraki	Tel:81-29-838-7007, Fax:81-29-838-7007) This clone is one of the 28K full-length cDNA clones from japonica rice.  This clone is one of the 28K full-length cDNA clones from japonica rice.  URL: http://cdna01.dna.affrc.go.jp/cDNA/ NNAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawadashira,N., Doi,K., Kishimoto,N., Yazaki,T., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M. FALS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
AKO71838 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE	JOURNAL PUBMED REFERENCE	АUТНО		TITLE JOURNAL	COMMENT

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aboratory in Riken: Adachi,J., A
T., Carninol,P., Fukuda,S., Hana
T., Hayashida,K., Hayatsu,N., Hir
Iida,J., Imamura,K., Imotani,K.
Kojima,Y., Kondo,S., Konno,H.
Matsuyama,T., Miyazaki,A., Mur.
, Nomura,K., Numsaski,R., Ohno,
akai,C., Sakai,K., Sakazume,N.,
Shibata,K., Shinagawa,A., Shirak
Tagami-Takeda,Y., Tagawa,A., I
aanaaka,T., Tomaru,A., Toya,T., Wa
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3G 929 | |-| | 1116

3T 989 | 3T 1176

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TA 610 | TG 794 | CA 670 | C 854

	- 2 -	555 AAAGTTCGTTACAGAGTAGAATTACAATTCTCAGAGGAAACCATGAAAC  431 AGGCAAATATGGTTTCTATGATGAATGCCGGAAATGC  615 ACTCAAGTGTATGGCTTCTATGATGAATGCCTCGGGAAATGC  616 ACTCAAGTGTATGGCTTCTATGATGAATGCTTCAGAAATACGAAATGC  617 AAGTACTTCACGGATCTGTTCGACTACCTGCCTCTGACAGCTCTCATGA		6/1 GATGATICGTTGTGGGGCATTTTCACCACGGGGGGGGGGTATATCTTT  855 GATGATCGTTGTGGGGTGGGGAATATCTCCACGGGGGGGG	35 35	911 CGGTCTTTCTCAGTTCGAACCAGCACCGCGGCAAAGTGAACCAGATGT 1095 CAGAATTTCTTCAGTTGACCCAGCCCCAGGCAAATTGAGCCTGATAC 971 ACTCCTGATTACTTTCTGTAA 991 1155 ACTCCAGATTATTTTTTTTTTTAA 1175	10  AF107464  ION Hevea brasiliensis serine/threonine protein phosphat (PP2A) mRNA, complete cds.  ON AF107464  AF107464. GI:3986749	Hevea brasiliensis  Hevea brasiliensis  Rukaryota; Viridiplantae; Streptophyta; Embryophyta;  Bukaryota; Viridiplantae; Streptophyta; Embryophyta;  Bukaryota; Viridiplantae; Streptophyta; Core e rosids; Gurosids I, Malpighiales; Euphorbiaceae; Crc  Micrandreae; Hevea.  Micrandreae;
q	S G S	90 OV	a & a & a	6 6 6 6	6	B & B &	RESULT 10 AF107464 LOCUS DEFINITION ACCESSION VERSION	ACT WOULD SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE
Db 1177 AATTTTCGTATAT 1189	RESULT 9 AB039917 LOCUS AB039917 1475 bp mRNA linear PLN 15-WAR-2000 DEFINITION Vicia faba vfPP2Ac-2 mRNA for type 2A protein phosphatase-2,	ACCESSION AB039917. AB039917.1 GI:7248360 VERNORDS VEPPEAGC-2: type 2A protein phosphatase-2. SOURCE Vicia faba (fava bean) ORGANISM Vicia faba Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; robids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciaee;	Vicia.  Vicia.  1 (bases 1 to 1475)  AUTHORS Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.  TITLE Type 2A protein phosphatase from guard cells of Vicia faba JOURNAL Published Only in DataBase (2000)  REFERENCE C (bases 1 to 1475)  AUTHORS Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.  TITLE Direct Submission JOURNAL Submitted (08 MAR-2000) Toshinori Kinoshita, Kyushu University, Graduate School of Sciences; Ropponmatsu 4-2-1, Fukuoka, Fukuoka	Parono, vagan (E-mari:Cosnircosmicox.nc.ryusnu.ac.)p, Tel:81-92-726-4763 (ex.4763), Fax:81-92-726-4644)  Location/Qualifiers 1. 1475  / organism="Vicia faba" /mol type="mRNA" /db xref="taxon:3906" /dev stage="guard cell protoplasts" /dev stage="mature"	/ note="synonym:vicia faba L."  gene	/protein_id="BaA92698.1" / db_xref="afg:1724836." / db_xref="agg.1724836." / translation="MPSGADLDROIEHLNBCKPLTESEVKALCDGARAIIUVEEWNUQP / translation="MPSGADLDROIEHTNYLEMGDYUDRGYYSVETUTILIVALKV RYRRRITILIKGHHESKOJTQVYGEYDELEKRYGANUVMEFTDLEPYLEPLFALISGUV FCLHGGLSPSLDTLDNIRALDRICGRYGHTGPROFILWSDPDDRCGWGISPRGGGTTFG QDIASQFNHTNGLSLISRAHQLVMEGYNWAQEKNVYTVFSAPNYCYRCGNNAAILEIG ENNOQNFLQFDPAPRQIEPDTTRKTPDYFL"	cch al Similarit 705; Conse	Oy         71 ATGCCGTCATATGCAGATGTAGACCGCAGATAGACCGGTGCGAGGCGTTG         130           19

CC 850 | CA 1034

AT 730 || AT 914 || TT 790 || FT 974

AT 910 | | AT 1094 AG 970 | AA 1154

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phyta; edons; e;

۷۷	725 CAAGATATIGCAGAGCAGTICAATCATACCAATGGTCTAAGTTTGGTTGC	1C 784
Dp 8	808 CAGGATATAGCTGCTCAATTCAACCATACCAATGGGCTCACTCTGATTTC;	1¢ 867
Oy 7	785 CAGCTTGTGATGGAAGGATACAATTGGTGCCAGGATAAAATGTTGTCAC	3T 844
Db 8	868 cagcicgicaiggaaggalacaaciggigicaggaaagaaigiggilac	3T 927
δ,	845 GCCCCCAATTACTGTTACCGCTGTGGGAACATGGCCGCCGTAATGGAGAT,	3A 904
Dp qu	928 GCACCAAACTATTGCTACCGGTGTGGAATTATGGCTGCAATTCTCGAGAT"	₹C 987
δ	905 ATGAATCGGTCTTTTCTTCAGTTCGAACCAGCACGCGGGAAAGTGAACC	.G 964
qq	988 ATGGCCCAGAACTTCCTTCAATTTGATCCTGCACCTCGGCAAATTGAACC	1G 1047
ζ	965 CGGAAGACTCCTGATTACTTTCTGTAA 991	
Db 10	048 cGCAAGACCCCTGATTTTTTATAA 1074	
RESULT 11 ATHPRPHB LOCUS DEFINITION ACCESSION	thalia	'R-1993
VERSION KEYWORDS SOURCE	M96733.1 GI:166822 protein phosphatase. Arabidopsis thaliana (thale cress)	
OKGANISM	Arabloopsis Lialiana Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core en rosids; eurosids II; Brassicales; Brassicaceae; Arab	ohyta; adons;
REFERENCE AUTHORS	1 (bases 1 to 1264) Arino, J., Perez-Callejon, B., Cunillera, N., Camps, M., Arino, J., Perez-Callejon, B., Cunillera, N., Camps, M.,	. and
TITLE	Feffer, A.  Protein phosphatases in higher plants: multiplicity of phosphatases in Arabidopsis thaliana Plant Mol. Biol. 21 (3), 475-485 (1993)	3 <b>A</b>
PUBMED	8382968 Original source text: Arabidopsis thaliana (library: young adult in flowering stage whole plant (including mann	3T10) 3DNA to
FEATURES		
	/orga /mol /db/x /tiss /dev_ /dev_	
S	1181038 /function="dephosphorylation of Ser-P and Ti /note="putative" /codon start=1	"dues"
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ORIGIN	ENMEQNFLQFDPAPRQVEPDTTRKTPDYFL"	
Query Match Best Local S Matches 708	ch 42.1%; Score 574.2; DB 15; Length 1: 1. Similarity 76.0%; Pred. No. 1.2e-161; T08; Conservative 0; Mismatches 223; Indels	3 0;
ζ	61 GGTTGGGACAATGCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC	1G 120
Db 1	108 dcTTTTCAAGATGCCGTCGAACGGAGATCTCGACCGTCAGATCGAGCAGC	rG 167

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TG 120 || TG 247

GT 180 || |GT 307

TA 300

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 12 AY059847 LOCUS DEFINITION

Stanford University, 855 California Avenue, Palo Alt. USA  USA  e-mail for correspondence: arab@sequence.stanford.ed  RIKEN Genomic Sciences Center (GSC) members carried ( collection and clustering of RAFL cDNA (RAFL cDNA :  Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, Hayashizaki, Y. and Shinozaki, Y.	The Salk, Stanford, PGEC (SSP) Consortium members ca: : the sequencing and annotation of the RAFL cDNAs: Southwill Nguyen, M., Karlin-Neumann, G., Lam, B., Miranda, M., P. Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chu Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shin: Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.	Southwick, equally to (SSP/Stanf Irce	/clone="Ul5346" /ccotype="Columbia" /note="This clone is in pENTR/SD-dTopo Th. :loned /note="This clone is in pENTR/SD-dTopo Th. :loned a template" a template" 1. :1092 /gene="At1g10430" /note="synonym: T10024.4" CDS /gene="At1g10430" /codon_start=1		Query Match 42.0%; Score 573.8; DB 15; Length 1. Best Local Similarity 76.4%; Pred. No. 1.5e-161; Matches 704; Conservative 0; Mismatches 217; Indels 3 0;	1	61 TCGGAGGGATGTGAGACCTTTGCGATCAGGGAGGATCTTGTT  191 AACGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCGGTGACATCCTTGT  121 AATGTTCAGCGGTGAAGTGTCCTGTTAGCGTTTGCGGTGACATCCAGG  251 GATCTCATCGAGGTTTTCCGCATAGGAGGCACACACACAC	181 GACCTTATTGTTTTTGTTGGTGGCACGCTCCTGATACTAACTA
CCAGTTTTATGACCTTATTGAGCTCTTTCGTATCGGTGGCAACGCTCCTGATACTAACTA		660 600 FEATURES 660 SOUICE	GTCTCAATCATCATCTGGAGGGATTTCACCACGGGTCCGGTTATACTTT 720  GTCTTCATCACATGATCGATCTGGAGGGGATTTCACCACGGTTATACTTT 720  GTCTTCATCCTCATCATCGATCTGGATCGGAGATATCTCCACGGGTTATACATT 847  GGTCTAATCATCACAGATCTAATCATACCAATGGTTCATCACGTTCATCACGTC 780	CAGTGCCCCCAATTACTGTTACCGCTGTGGGGAACATGGCCGCCATAATGGAGATAGA 900	1088 TACTCGGAAGACCCCTGATTATTTTTGTGA 1118  Best Local 8  Matches 70	S thalians similar to protein phosphatase type 2A  MRNA, complete cds.  Oy 7	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W., Db 241 Dbirect Submission

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RESULT 13 AY093267 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

EEWNVQP LLVALKV ALIESQI GAGYTFG

CT 111 | |TT 347

AC 171 | | |GC 407

GT 351 || GT 587

TT 591 | CT 827 | GA 651 | | GA 887

GG 711 |-| GG 947 GT 771

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FA 610 | |G 692

3A 670 | 3C 752

VT 730 | |C 812

7T 790

3C 850 3A 932

VT 910 | VA 992

CDS

971 ACTCCTGATTACTTTCTGTAA 991 || || || || || || || || || 1 1053 ACCCTGATTATTTTTGTGA 1073

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GenCore version 5.1.6
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Run on:

December 9, 2005, 04:43:25; Search time 819 Seconds (without alignments) 11107.821 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-764-259-8 1365 1 ggcgttaacgcgcggaggag......tatggcatgctcgagctcgc 1365

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4996997 seqs, 3332346308 residues Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2005s:\*

## SUMMARIES

* Query
Match Length DB
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0 1365
7 1732
2 1386
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7 1298
42.5 1422
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41.1 1267
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                        New transgenic plant cell transformed by phosphatase stress protein coding nucleic acid whose expression in the cell re increased tolerance to environmental stress compared to wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a transgenic plant cell (I) transf
                                                                                                                Physcomitrella patens; PHSRP; phosphatase stress related PP2C; enzyme; transgenic; plant; stress tolerance; gene;
                                                                                          Physcomitrella patens PP2A-4 encoding cDNA SEQ ID NO 8.
                                                                                                                                                                      Location/Qualifiers
71. .991
/*tag= a
/product= "PP2A-4"
                      ABN81332 standard; cDNA; 1365 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Fig 2; 106pp; English.
                                                                                                                                                                                                                                                                                                    07-APR-2000; 2000US-0196001P.
                                                                                                                                                                                                                                                                              06-APR-2001; 2001WO-US011253
                                                                                                                                                                                                                                                                                                                          (BADI ) BASF PLANT SCI GMBH.
                                                                    (first entry)
                                                                                                                                                   Physcomitrella patens.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-508562/54.
P-PSDB; ABB77578.
                                                                                                                                                                                                                                 WO200246442-A2
                                                                    02-SEP-2002
                                                                                                                                                                                                                                                       13-JUN-2002.
                                             ABN81332;
RESULT 1
            ABN81332
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phosphatase stress-related protein (PHSRP) coding nucleic acid (ABN81330-ABN81334), where expression of the nucleic acid in the plant cell results in increased tolerance to an environmental stress as compared to a wild type variety of the plant cell. PHSRP encoding genes are useful for identifying Physcomitrella patens and related organisms, as markers for specific regions of the genome, mapping of genomes of organisms related to patens, identification and localisation of PHSRP regions related for function, modulation of patens sequences of interest, evolutionary studies, determination of PHSRP regions required for function, modulation of the transmembrane transport of one or more cell functions, modulation of the transmembrane transport of one or more cell functions, modulation of stress resistance. The gene is also useful for identifying and/or cloning PHSRP homologues in other cell types and organisms, for identifying and organisms as being polynucleotide of the invention  Sequence 1365 BP; 337 A; 282 C; 373 G; 373 T; 0 U; 0 Other;	_	1 GGCGTTAACGCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CONTROL	301 CTTGTTCATGGGCGACTATGTGGATCGTGGATATTATTCTGTCGAGACTGTGTCGCTCTT 360	GATGTTTGGAAGTACTTCAGGATCTGTTGATTGCTGCGAGGAGTTGCTGAGAGCTCTCTGAGAGCTCTCTGAGAGCTCTCTGAGAGCTCTCTGAGAGCTCTCTGAGAGCTCTCTGAGAGCTCTCTGAGAGCTCTCTGAGAGCTCTCTGAGAGCTCTTGATTGA
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J	Qy 781		FT 840
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Ŭ		CAGTGCCCCCAATTACTGTTACCGCTGTGGGAACATGGCCGCCATAATGG;	0
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J 1	Oy 901	. AACAATGAATCGGTCTTTTCTTCAGTTCGAACCAGCACGCGGGGAAAGTG. 	3T 960
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J -	Oy 961	. GACCGGAAGACTCCTGATTACTTTTCTGTAAACATGGCCTATACATGGTA(	FT 1020
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<u> </u>	н,	CCCTCATGATCTAGTAGTATGAAGTTATCTTTTGAAGTGTTTGTT	4 4
-	108		7.7
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			126
		CTGCGACAAGAGGAGCAGTGTCAATGGTTGCAAGGGTTATAGGTATTAGG	26
	Qy 1261		\C 1320
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	Qy 1321	AACGITCATCICCACACCTACTGIATATGGCATGCTCGAGCTCGC 1365	
-	Db 1321		
	.623	9 standard; cDNA; 1365 BP.	
	AC ABX16239	10	
· - '	H.	-2003 (first entry)	
/	DE P. patens	ns protein phosphatase PP2A-4 cDNA.	
,	KW Plant; K KW phosphat KW Balt toj	Plant; ss; gene; PP2A-4; protein phosphatase; PHSRP; cold; phosphatase stress related protein; environmental stress; d: salt tolerance.	<i>(</i> C)
		comitrella patens.	
,	AX FH Key FT CDS FT	Location/Qualifiers 71991 /*tag= a /product= "PP2A-4"	
., _	XX PN US20021!	002152502-A1.	
	XX PD 17-OCT-2002	2002.	
	XX PF 06-APR-:	APR-2001; 2001US-00828302.	
	PR 07-APR-200	2000; 2000US-0196001P.	
	(//	DA COSTA E SILVA O.	

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The invention relates to a transgenic plant cell transformed by a Phosphatase Stress-Related Protein (PHSRP) coding nucleic acid. The expression of the nucleic acid in the plant cell results in increased tolerance to an environmental stress (e.g. salt tolerance, cold and drought) as compared to a wild type variety of the plant cell, a seed conduced by the transgenic plant comprising the novel plant cell, a seed produced by the transgenic plant comprising the seed is true breeding for an increased tolerance to environmental stress as compared to a wild type variety of the plant cell, an agricultural product produced by the plant cell, an agricultural product produced a recombinant expression vector comprising the nucleic acid, and producing a transgenic plant containing PHSRP nucleic acid. The transgenic plant cell transformed by a Phosphatase Stress-Related Protein (PHSRP) coding cucleic acid is useful for modifying stress tolerance of a plant. The present sequence encodes the PHSRP, protein phosphatase, PP2A-4
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                                                                                                                                                                        New transgenic plant cell transformed by a Phosphatase Stress-Related Protein (PHSRP) coding nucleic acid, useful for modifying stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGTTAACGCGCGGAGAGAGCGGATCGGTTAGGGTTTGGTGCCAGGGGGAGGGCAGA
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                                                                                        Ishitani
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                                                                                      Chen R,
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                                                                                      Van Thielen N,
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                     Da Costa E SilvaO, Bohnert HJ,
                                                                                                                                                                                                                                             Claim 18; Fig 2C; 79pp; English
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Best Local Similarity 100.
Matches 1365; Conservative
 BOHNERT H J.
VAN THIELEN N.
                                                                                                                                                                                                            tolerance of a plant.
                                                                                                                     WPI; 2003-198392/19
P-PSDB; ABG74203.
                                                  ISHITANI M.
                                    CHEN R
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(VTHI/)
(CHEN/)
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in meletronic form from the UB patent office at available in electronic form from the UB patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme compositions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ingnin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 AGGCGATCCTCATGGAGGAGTGGAACGTACAGCCCGTGCGCTGCCCCGTCACTGTGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 GGTAGAGCCGCAGCGCGATGCCGTCGCACGCGGATCTGGACCACCACAGATCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGACATCCATGGCCAGTTTCATGATCTCATCGAGCTTTTCCGCATAGGAGGCAAGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
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Pred. No. 3.8e-175;
0; Mismatches 219; Indels
                                                                                                                                                                                                                                                                                                                                                                              Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                              Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 35277; 15pp; English
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05-NOV-2001; 2001US-00985678.
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nes 728; Conserv
                                                                                                      US2004034888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               improving yield.
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ZHOU Y.
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                                                                    Unidentified
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(SCRE/)
(TABA/)
(CAOY/)
                                                                                                                                                                                                                                                        (LIUJ/)
(ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                              Liu J,
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BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
OSPP2A-2; OSPP2A-3; plant tolerance; environmental stress; )
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/product= "protein phosphatase stress-relat"
polypeptide"
                                                                                                                                                                                                    CATTAGATCACATCCGAGCCCTAGATCGTATTCAAGAAGTGCCGCACGAG
                                                                                                                                                                                                                    CATTGGATAATATCCGCCCCTTGATCGCATACAAGAGGTCCCACATGAA
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                  cadacaccaactracereritariogocoarracoreoacearocaacrae
                                                                                                                     AGTATGGAAATGCGAATGTTTGGAAGTACTTCACGGATCTGTTCGACTAC
                                                                                                                                TGGTTGCACGTGCTCACCAGCTTGTGATGGAAGGATACAATTGGTGCCAG
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CCGACACGAACTACTTGTTCATGGGCGACTATGTGGATCGTGGATATTAT
                                                          CTGTGTCGTTGTTAGTGGCTCTAAAAGTACGTTATAGAGACAGAATCACA
                                                                             GGAACCACGAGGCAGGCAGATTACGCAAGTATATGGTTTCTATGATGAA
                                                                                         GAAATCATGAGGGAGAAAAAAAACTCAAGTGTATGGCTTCTATGATGAA
                                                                                                                                                            GTGATCTACTCTGGTCTGATCCAGATGATCGTTGGATGGGGCATTTCA
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Protein phosphatase stress-related polypeptide; PPSRP; PpPE BnPP2A-1; BnPP2A-2; GmPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3; OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress; drought; salinity; cold; enzyme; gene; ss.
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  461 TATGGCTTCTATGATGATGCTTGAGAAATATGGAAATGCGAATGTCTC
                                                                    Acadacridirrdarrarrecercescercarreagaercagai
                                                                                                                                                              carcaccricricritricataracacracaracaricacari
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                                            ACGGATCTGTTCGACTACCTGCCTCTGACAGCTCTCATTGAGCACGAGAI
                                                                                                                           CATGGTGGTCTCTCCATCGCTCGACACATTAGATCACATCCGAGCCCT
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                                                                                                                                                                                                                                                                                                                                                                               CAGTICAATCATACCAATGGTCTAAGTTTGGTTGCACGTGCTCACCAGCT
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                                                                                                                                                                                                            CAAGAAGTGCCGCACGAGGCCCCGATGTGTGATCTACTCTGGTCTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a protein phosphatase stress-related
polypeptide (PPSRP). The specification describes PPSRP polypeptides
designated PpPP2A-1, PPPP-1, BnPP2A-2, BnPP2A-3, GmPP2A-1,
GmPP2A-2, GmPP2A-3, OSPP2A-1, OSPP2A-1, BnPP2A-2, BnPP2A-3, GmPP2A-1,
GmPP2A-2, GmPP2A-3, OSPP2A-1, OSPP2A-1, BnPP2A-3, derived from
C Physicomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP
C tolerance to an environmental stress such as drought or increased
c alinity and cold. They are also useful in identification and
C salinity and cold. They are also useful in identification and
C salinity and related organisms, mapping of genomes of organisms
c related to the above species, in a evolutionary and polypeptide
c structural studies, in determination of PPSRP regions required for
function, modulation of PPSRP activity, modulation of metabolism of one
c or more cell functions and transmembrane transport of one or more
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                                                                                                                                                                                                                                                                                                           New protein phosphatase stress-related polypeptide coding nucleic acid, useful for modulating plant's tolerance to an environmental stress such as drought, increased salinity and cold.
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43.2%; Score 589.6; DB 10; Length 1386;
Best Local Similarity 75.4%; Pred. No. 5.2e-173;
Matches 733; Conservative 0; Mismatches 239; Indels 0;
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P-PSDB; ABP98034.
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abepass/29.  ein phosphatase stress-related polypeptide coding mucor modulating plant's tolerance to an environmental sht, increased salinity and cold.  Page 87-88; 107pp; English.  Page 87-88; 107pp; English.  Find (PPSRP). The specification describes PPSRP polypered (PPSRP). The specification describes PPSRP polypered (PPSRP). The specification describes PPSRP polypered (PPSRP). PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-2, BnPP2A-3, Garthed PPP2A-1, OSPP2A-1, OSPP2A-2, or OsPP2A-1, OSPP2A-1, OSPP2A-1, OSPP2A-2, or Osppa, or the total and polynucleotides are useful for modulating pletton of Physcomitrella patens, Brassica napus, Glycintion of Physcomitrella patens, Brassica napus, Glycintion and related organisms, mapping of genomes of orginal studies, in determination of PPSRP activity, modulation of metabolation of perseptions required.	or more c component Sequence Query Match Best Local S Matches 719 81 108 118	Db 201 descentrated descentrated and control of the

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polypeptides and polynucleotides are useful for modulating pla tolerance to an environmental stress such as drought or increase almity and cold. They are also useful in identification and localization of Physcomitrella patens. Brassica napus, Glycine Oryza sativa and related organisms, mapping of genomes of organ related to the above species, in a evolutionary and polypeptid structural studies, in determination of PPSRP regions required function, modulation of PPSRP activity, modulation of metaboli or more cell functions and transmembrane transport of one or m
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	¥ & &	Hybridisation assay; gen protein identification;	Hybridisation assay; genetic mapping; gene expression contr protein identification; signal transduction pathway; metabc	hway;
	¥ X	promoter; termination se	equence; corn; ss.	•
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FTGCGGTGACA 233	Z,	EP1033405-A2.		
CTGCGGCGACA 338	<b>S</b>	06-SEP-2000.		
GCCCCGACA 293	<b>₹</b> & }	25-FEB-2000; 2000EP-00301439	11439.	
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Query Match 42.5%; Score 579.6; DB 3; Length 14: Best Local Similarity 74.8%; Pred. No. 7.1e-170; Matches 726; Conservative 0; Mismatches 244; Indels

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18-OCT-2000 (first entry)

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Hybridisation assay; genetic mapping; gene expression contr
protein identification; signal transduction pathway; metabc
promoter; termination sequence; corn; ss.
       Zea mays DNA fragment SEQ ID NO: 44101.
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99US-0123180P

99US-012548P

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       AGACTGTGTCGCTCTTAGTGGCCCCTGAAGGTGCGGTATAGGGATGAGATCAAATCTTGC
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                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 27232
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99US-0123180P.
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  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 39005.
           AAC43368 standard; DNA; 921 BP
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61 GGTGAAGCAGACGTGAAGATCCTTTGCGATCAAGCTAAAGCGATTCTTGT"	191 AACGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCGGTGACATCCATGGG			241 GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTGTATT: 371 AAGGTGCGGTATAGGATAGATCACAATCTTGCGAGGGAACCACGAGG		431 ACGCAAGTATATGGTTTCTATGATGAATGCCTGCGGAAGTATGGAAATGC 	491 AAGTACTTCACGGATCTGTTCGACTACCTGCCTCTGACAGCTCTCATTGAA 	551 TTTTGTCTTCATGGTGGTCTGTCTCCATCGCTCGACACATAGATCACAT	611 GATCGTATTCAAGAAGTGCCGCACGAGGGCCCGATGTGTGATTTACTCTGA	671 GATGATGGTTGTGGATGGGGCATTTCACCAGGAGGTGCGGGTTATACTTT"	731 ATTGCAGAGCAGTTCAATCATCAATGGTCTAAGTTTGGTTGCACGTGC	791 GTGATGGAAGGATACAATTGGTGCCAGGATAAAAATGTTGTCACAGTTTT: 	851 AATTACTGTTACCGCTGTGGGGAACATGGCCGCCATAATGGAGATAGAT	911 CGGTCTTTTCTTCAGCTCCGCGCGCAAAGTGAACCAGATGT 	971 ACTCCTGATTACTTTCTGTAA 991                            901 ACCCCTGATTATTTTGTGA 921	RESULT 12 ABZ12900 ID ABZ12900 standard; DNA; 921 BP.	ABZ12900; 21-JAN-2003 (first entry)	Arabidopsis thaliana stress regulated gene SEQ ID NO 705. Arabidopsis thaliana; plant; gene; stress; transgenic; ds.	
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polypeptide"
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                                                            TICTGTTTGCATGGAGGCCTTTCACCTTCTCTGGATACTCTTGACAATAI
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                                                                                                                                                                   GATCGAATACAAGAGGTTCCACACGAAGGACCAATGTGCGATCTACTCTG
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                                                                                                                  GATCGTATTCAAGAAGTGCCGCACGAGGGCCCCGATGTGTGATCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabiotosis thalians stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 ATGCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGCTGTCGGAGTGCAAGCCGTTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGGTGGAGGAGTGG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGAAGCAGACGTGAAGATCCTTTGCGATCAAGCTAAAGCGATTCTTGTTGAGGAATAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGCAAGTATATGGTTTCTATGATGAATGCCTGCGGAAGTATGGAAATGCGAATGTTTGG 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AATCTICAACCGGTTAACTGTTCCGGTTACGGGCGGTATCCATGGCCAGTTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 144; SEQ ID NO 705; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 921 BP; 252 A; 183 C; 225 G; 261 T; 0 U; 0 Other;
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                               24-AUG-2001; 2001WO-US026685
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as drought, increased salinity and cold. Claim 1: Page 74-75: 107mp: English	ò	780 CTCA	CTCACCAGCTTGTGATGGAAGGATACAATTGGTG
iam ij rage (1-70) 10/pr) migilom. S present semjence encodes a protein phosphatase stress-related	qu	859 CACA	
* present sequence encodes a procent prospatates briefs-related. -ypeptide (PPSRP). The specification describes PPSRP polypeptides iignated PpP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3, GmPP2A-1, PPZA-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived from	S S	840 TCAGTGC           919 TTAGCGC	I
Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP polypeptides and polymelectides are useful for modulating plant tolerance to an environmental stress such as drought or increased salinity and cold. They are also useful in identification and	ko a		AAACAATGAATCGGTCTTTTCTTCAGTTCGAACC 
localization of Physcomiffella patens, Brassica napus, Glydine max or Oryza sativa and related organisms, mapping of genomes of organisms related to the above species, in a evolutionary and polypeptide structural studies, in determination of PPSRP regions required for function, modulation of PPSRP pregions cequired for or more cell functions and transmembrane transport of one or more	\$ B	960 TGAC    1039 CTAC	tgacgcggaagactcctgattactttctgtaa 
components Sequence 1243 BP; 337 A; 258 C; 299 G; 349 T; 0 U; 0 Other;	SUL C45	14 30 AC45630	standard; DNA; 1259 BP.
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19		Hybridisation	tic mappi
120 GCAAGCCGTTGTCGGAGTTGGAGGTCAAGAACCTATGTGATCAAGCTCGGACGATCTTGG 179	XXXX	protein ident promoter; ter	<pre>lentification; signal trans termination sequence; ss.</pre>
199 GIRARACCOII CILCOMAGGICGARGE GRAGAICGITGI GCGAGCARGCARGCARGCARICCAII LIGG 200 180 TIGGAGGAGGTGGAACTGCAGCAGGAAGGAGTGTCTTGTCACACATATACAGATGACATACAGAGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA		Alabidopsis chailaha Epinaaans-ao	יומד דמוזמ .
TGGAGGAGAGGAATGTTCAGCCGGTTAAGTGTCCGGTCACCGTCTGCGGCGACATCCACG 31		06-SEP-2000.	
240 GCCAGTTTCATGATCTCATCGAGCTTTTCCGCATAGGAGGCAAGGCGACGCCGACACGACT 299 119 GCCAGTTTTTACGATCTTTTTTTTTAAGATCGTAGTTTTTTTT		25-FEB-2000;	0
ACTTGTTCATGGGCGACTATGTGGATCGTGGATATTATTCTGTCGAGACTGTGTCGCTCT	# # #	05-MAR-1999; 09-MAR-1999; 23-MAR-1999;	990S-0123180P. 990S-0123548P. 990S-0125788P.
379 AICTCTTCATGGGCGATTACGTAGATCGAGGGTATTATTCTGTGGAGACAGTCTCGCTCT 438 360 TAGTGGCCCTGAAGGTGCGGTATAGGGATAGGATCACAATCTTGCGAGGGAACCACGAGA 419		25-MAR-1999; 29-MAR-1999; 01-APR-1999;	
		06-APR-1999; 08-APR-1999;	
420 GCAGGCAGATTACGCAAGTATATGGTTTCTATGATGAATGCCTGCGGAAGTATGGAAAGT 479		18-APK-1999; 19-APR-1999; 21-APR-1999; 23-APB-1999;	
GCCGCCCAMALIACICAMOLGIALGGALILITAGAGGAGCCILGAGAAMALIALGGGAAALG CGAAAGATTTGGAAGTACTTCACGGAACTGCTTGGAGACTACCTTGCCTTCTGACAAGATGATTG		23-AFR-1999; 23-AFR-1999; 28-AFR-1999;	
CTAATGTCTGGAAACACTTCACGACCTTTTTGATTATCTTCCTCTTACAGCTCTCATCG		30-APR-1999; 30-APR-1999;	
AGCACGAGATTTTTGTCTTC		04-MAY-1999; 05-MAY-1999; 06-MAY-1999;	
AGAGTCAGGTTTTCTGTTTACATGGAGGCTCTCACCTTCTTTAGATACACTTGACAAAA		06-MAY-1999; 07-MAY-1999;	
600 TCCGAGCTCTRATCTCT 659 610 TCCGAGCTCTRATCTCT 659 679 TCCGTTCTCTAGATCGAAGAGTTCCACATGAAGACCTATGTGATCTGTTAT 738		11-MAY-1999; 14-MAY-1999; 14-MAY-1999;	
		14-MAY-1999; 14-MAY-1999; 18-MAY-1999;	
GGTCCGATCCAGATGATCGATGCGGTTGGGGAATATCTCCTCGTGGCGCAGGCTACACGT 79		19-MAY-1999; 20-MAY-1999;	
720 TTGGTCAAGATATTGCAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGCACGTG 779	# #	21-MAY-1999; 24-MAY-1999;	

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VA 192 used: ic 132 ed and lants that A-A 5=5 The invention relates to identifying a stress condition to cell has been exposed, comprising: (a) contacting nucleic a representative of expressed polynucleotides in the plant cell array or probes representative of the plant cell genome; and detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful it production of transgenic plants, cells and seeds and in prowing increased tolerance to abiotic stress. The present sequence of an Arabidopsis thaliana stress regulated gene (ABZ12196.) In methods of the invention. Note: The sequence data for the not respresented in the printed specification but is based on information supplied to Derwent by the European Patent Officential and seeds and second or information supplied to Derwent by the European Patent Officential and seasons. Identifying a stress condition to which a plant cell has ber producing plants with increased tolerance to these abiotic Length 92. rgaaacggaggrgaagargrrgrgrgaggacgcaaagacgarrcrrgrgg CGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCGGTGACATCCATGGCC 126 refrchaccestraaristccstraccerciscssisararccacss rcraarcgagcrirrrcgrarcgrggrrcrrcrccrgaracraarrarc TGATTATGTTGATCGAGGGTATTATTCTGTGGAGACAGTCTCACTTTTGG 73 GCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGCTGTCGGAGTGCA GCCGGCGACCGGAGATATCGATCGTCAGATCGAGCAGCTTATGGAGTGTA 133 GGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGGTGG TCTCATCGAGCTTTTCCGCATAGGAGGCAAGGCGCCCGACACGAACTACT CGACTATGTGGATCGTGGATATTATTCTGTCGAGACTGTGTCGCTCTTAG Claim 144; SEQ ID NO 571; 577pp + Sequence Listing; English Sequence 924 BP; 246 A; 183 C; 212 G; 283 T; 0 U; 0 Other; Arabidopsis thaliana, plant, gene, stress, transgenic, 39.0%; Score 531.8; DB 6; 73.7%; Pred. No. 5e-155; tive 0; Mismatches 242; thaliana stress regulated gene (SCRI ) SCRIPPS RES INST. (SYGN ) SYNGENTA PARTICIPATIONS AG. Wang X, 24-AUG-2000; 2000US-0227866P. 26-JAN-2001; 2001US-0264647P. 22-JUN-2001; 2001US-0300111P. 24-AUG-2001; 2001WO-US026685 (first entry) Best Local Similarity 73.73 Matches 677; Conservative Harper JF, Kreps J, Arabidopsis thaliana WPI; 2002-304127/34. WO200216655-AZ. Arabidopsis 21-JAN-2003 28-FEB-2002 246 193 253 Query Match à

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9	Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y.,	:1,K.,
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	transcriptome and Arabidopsis thaliana: implication	plant
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ä	12808149	
	Contact: Tadasu Shin-i	
	Center For Genetic Resource Information	
	of Genetics	
	IIII Yata, Mishima, Shizuoka 411-8540, Japan	
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	that was in vivo excised from a 1-81.0 phase vector (	ייי פידם
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	vector(5'- gAgAgAgAgAgATCCAACCCTggAgAgTTTTTTTTTTT	was
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	Protonemata were blended by the POLYTRON, and then c	l on
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	These clones are available from RIKEN Bio Resource (	

RESULT 2 BJ5598448/c LOCUS LOCUS DEFINITION BJ598448 normaliz Caulonemata and r Subsp. patens cDN ACCESSION BJ59848.1 GI:37 KEYWORDS SOURCE Physicomitrella pa ORGANISM Physicomitrella pa Bryopsida; Funari REFERENCE I (bases 1 to 74 AUTHORS Nishiyama, 7., Ful		JOURNAL Proc. Natl. Acad. PUBMED 12808149 Tadasu S COMMENT COntact: Tadasu S CONTACT: Tadasu S CONTACT: Tadasu S Anticonal Institut 1111 Yata, Mishim	Tel: 81-559-81-68 Fax: 81-559-81-68 Email: tshini@gen A backbone of the that was in vivo	2001). 5' end of to Sall site of t ligated to BamHI vector(5'- gAgAgA	1860 as a 185 3 5'-ggTTTTCgAGTCAT 5'-hairpin primer AGGCCAATTCGGCCAG	ampinisa wil co CDNA library was Nishiyama et al. Protonemata were	These clones are (http://www.brc.r	(ACLD://MOSS.ALDD FEATURES 1.0cation Source 1.740 /organis	######################################	rhizoid- rhizoid- /clone_l chlorone	Query Match Best Local Similarity 99.	618 TTC	678
(http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physconitrella EST clones is available at the PHYSCObase (http://moss.nibb.ac.jp): Location/Qualifiers 1. 746 //organism="physcomitrella patens subsp. patens" //mol_type="mRNA" //mol_type="mRNA" //mol_type="mRNA" //mol_type="mRNA" //mol_type="mRNA" //mol_type="mixture of chloronemata, caulonemata and malformed buds" //clone="ppub3cilo" //tissue type="mixture of chloronemata, caulonemata and malformed buds" //clone lib="normalized full length cDNA library, chloronemata, caulonemata and malformed buds"	Query Match 54.3%; Score 741.4; DB 3; Length 746; Best Local Similarity 99.9%; Pred. No. 3.9e-208; Matches 742; Conservative 0; Mismatches 1; Indels 0; Gaps	Oy         615 GTATTCARGAAGTGCCGCACCCGATGTGTGATCTACTCTGGTCTGATCGAGATG         674	DD 686 ATCGTIGIGGAIGGGGIAITICACCACGAGGIGCCGGITAIACTITIGGICAAGAIAIIG 627  Qy 735 CAGAGCAGIICAAICAIACCAAIGGICIAAGIITIGGIIGCACCAGCCIIGIGA 794  DD 626 CAGAGCAGIICAAICAIACAIAGGICIAAGIIIIGCIIGC	Qy 795 TGGAAGGATACAATTGGTGCCAGGATAAAAATGTTGTCACAGTTTTCAGTGCCCCCAATT 854	OY 855 ACTGTTACCGCTGTGGGAACATGGCCGCCATAATGGAGTAGATGAAACAATGAATCGGT 914	Oy 915 CTTTCTTCAGTTCGAACCAGCACCGCGGAAAGTGAACCAGATGTGACGCGGAAGACTC 974	Oy 975 CTGATTACTTTCTGTAAACATGGCCTATACATGGTACCTTTTACTTAC	Oy 1035 TATAGTCACCTTCCATGGAAGCAGTTTGCCCCTGAATGAA	Qy 1095 FAGTATGAAGTTATCTTCTTTGAAGTGTTTGTTCCCTTTTTTAGTACTTGCTCCTCTGTT 1154	Oy 1155 CATTCATAAAGTTGCCTTCAGAACAACTGAGATGTTGTGAATGTTAACTGCGACAAGAGGA 1214	OY 1215 GCAGTGTCAATGGTTGCAAGGGTTATAGTGATTAGGGAAAGAAGGTAGCCACATGTTACTT 1274	Oy 1275 CAAATCGAFCAGACACTTCTATGGAAAAGAFGACGATGGTGGAAACAACGTTCAFCTCCA 1334	Oy 1335 CACCTACTGTATATGGCATGCTC 1357

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	coulonemata and rhizoid-like protonemata Physiconitre	ຜ
	subsp. parens cuna clone ppnnziniu i', mkwa sequence BJ598448	
VERSION KEYWORDS	BJ598448.1 GI:37840440 EST.	
	Physicomitrella patens subsp. patens	
ORGHINIS	" Filyscomitteria patens subsp. patens Bukaryota Viridijantae, Streptophyta, Embryophyta; Bukoneida, Bunidijae, Bunarialee, Bunariaceae, Dhve.	, , ,
REFERENCE	1 (bases 1 to 740)	s
AUTHORS	Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y.,	i, K.,
7.TTT.F	Kohara, Y. and Hasebe, M.	
	transcriptome and Arabidopsis thaliana: implication	plant
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2	
PUBMED COMMENT	12808149 Contact: Tadasu Shin-i	
	r For Genetic Resource Inform hal Institute of Genetics	
	1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856	
	Fax: 81-559-81-6855 Email: tshini@qenes.niq.ac.ip	
	A backbone of the vector is basically from pBluescri;	, (
	that was in vivo excised from a 1-ful phage vector () 2001). 5' end of the cDNA that was digested with Xho	
	to SalI site of the vector and the 3' end including : ligated to BamHI site of the	l was
	vector(5' - gAgAgAgAgAgAgCAACCCTggAgAgTTTTTTTTTTTTT	was
	5'-garrategarcardgerarcagaragaaaccgnnn	2nd
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	amplified with conventional T7 and T3 primers. This CDNA library was generated according to the method d	t th
	Nishiyama et al. (2003).	
	Protonemata were blended by the FOLTIKON, and then c the BCDATG medium for 13- 14 days under the continuo	Ö
	These clones are available from RIKEN Bio Resource C.	9
	(nctp://www.brc.riken.go.jp/lab/epg/index.ncml). of Physcomitrella EST clones is available at the PHY.	Dase
FEATURES	(http://moss.nibb.ac.jp). Location/Qualifiers	
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	ad . deeme	
	/sub_species≈"patens" /db_xref="taxon:145481"	
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	orotonemata"	1
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Oy         1158 TCATAAAGTTGCCTTCAGAACAACTGAGATGTTGTGAATGTAACTGCGACAAGAGGAGCA 1217           Db         212 TCATAAAGTTGCCTTCAGAACTGAGATGTTGTGAATGTAACTGCGACAAGAGGAGCA 153           Qy         1218 GTGCAATGGTTGCAAGGGTTAAGTGATTAGGAAAGAAGAAGAAGAAGAAGTAGCAATGTTACTTCAA 1277           Db         152 GTGTCAATGGTTGCAAGGGTTAATAGTGATTAGGGAAAGAAGAAGAAGAACTAGCACATTATTACTTCAA 93           Qy         1278 ATCGATCAGAGATTCTATGGAAAAGATGACGATGGTGGAAACAACATCATCTCCACAC 1337           Db         92 ATCGATCAGAGATTCTAATGGAAAAGATGACGAAGAAGAACAACGTTCATCTCCACAC 33           Qy         1338 CTACTGTATATGGCATGCTCGACTCGATGGTGGAAACAACGTTCATCTCCACAC 33           Cy         1338 CTACTGTATATGGCATGCTCGACTCGA 1365           Db         32 CTACTGTATATGGCATGCTCGAGTGGTGGAAACACGTTCATCTCCACAC 33           Cy         1318 CTACTGTATATGGCATGCTCGACTCGC 1365           Db         32 CTACTGTATATGGCATGCTCTGAGAGC 5	RESULT 4 BJ976562 BJ97662 BJ	Hasebe,M. Physcomitrella patens EST from young sporophytes with surroun archegonia Unpublished (2005) Contact: Tadasu Shin-i Contact For Mishima, Shizuoka 411-8540, Japan Tati: 18-1559-81-6856 Fax: 81-559-81-6856	stereomicroscope and their RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHYSCOBSES (http://moss.nibb.ac.jp).  Location/Qualifiers  Location/Qualifiers  1. 762  1. 762    Toganism="Physcomitrella patens subsp. patens"   mol type="mRNA"   sub_species="patens"     dol type="mRNA"   clone="pspspatiof"     clone="pspspatiof"     fissue_type="sporophytes (embryos) with surrounding archegonia"     dev stage="yorophytes cultivated for 3-4 weeks at 15C under short-day conditions"     clone_lib="ppsp full-length cDNA libary"	Query Match         53.8%; Score 734.8; DB 3; Length 762;           Best Local Similarity 99.3%; Pred. No. 3.6e-206;           Matches 758; Conservative 0; Mismatches 3; Indels 2; Gaps 2;           Qy         574 TCCATCGCTCGACATTAGATCACATCCGAGCCCTAGATCGTATTCAAGAAGTGCCGCA 633           Db         762 TCCATCGCTCGACATTAGATCACATCCGAGCCCTAGATCGTATTCAAGAAGTGCCGCA 703           Qy         634 CGAGGGCCCGAAGTGTATTCATCATCTCGTCTCGTCTCG

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       Email: tshini@genes nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-FiC phage vector (Carninci et al.
2001). 5' end of the cDNA that was digested with XhoI was ligated
to Sall site of the vector and the 3' end including polyA tail was
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vector(S'- aAgAgAgAgAgArCARCCTGGAGATTCGAGACTCGAGACTCGAGATCGGAGATCGGATTCGAGCTGGAGATCGGAGATCGGAGATCGGAGATCGGAGATTCGTCGAGACGGO, cDNA instert could be
amplified with conventional T7 and T3 primers. This full-length
CDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDATG medium for 13- 14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center
(http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database
of Physcomirrella EST clones is available at the PHYSCObase
(http://moss.nibb.ac.jp).
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/tissue_type="mixture of chloronemata, caulonemata
malformed buds"
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/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
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FERENCE AUTHORS	in-i,T., Seki ninci,P., Hay	i,K.,
TITLE	Notara, F. and HaseDE,M. Comparative genomics of Physcomitrella patens gameto transcriptome and Arabidopsis thaliana: implication evolution	plant
Z 🖾	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2 12808149	
MMENT	Contact: Tadagu Shin-1 Center For Genetic Resource Information National Institute of Genetics	
	1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855	
	Email: tshini@genes.nig.ac.jp A backbone of the vector is basically from pBluescri	
	that was in vivo excised from a 1-FLC phage vector (2001). 5' end of the cDNA that was digested with Xhc	et al. pated
	to sail site of the vector and the 3 end including ligated to BamHI site of the vertor(5'- abanHI site of the vertor(5'- abanHI site of the state of	T WAS
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transcriptome and Arabidopsis thaliana: implication evolution JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2 PUBMED 12808149 CONTACT: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yeta, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855	1: tshini@genes.nig.ac.jp choone of the vector is basically from pBl choone of the vector is basically from pBl choone of the vector and the 3' end incl is sie of the vector and the 3' end incl is sie of the vector and the 3' end incl is sie of the vector and the 3' end incl is sie of the vector and the 3' end incl is of the of the or(s'- gAghaghagharchacchacchaghagharchachaghagharchachaghagharchachagharc	Proconemata were blended by the PolyTYRON, and then c the BCDATG medium for 13-14 days under the continuor These clones are available from RIKEN Bio Resource C (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). of Physcomitrella EST clones is available at the PHY: (http://moss.nibb.ac.jp). FEATURES  Location/Qualifiers Source //moll.type="mRNA" //moll	ORIGIN  Query Match  Query Match  47.8%; Score 653; DB 3; Length 666;  Best Local Similarity 99.2%; Pred. No. 6.5e-182;  Matches 656; Conservative 0; Mismatches 5; Indels  Qy 705 GTGCCGGTTATACTTTTGGTCAGATTGCAGAGCAGTTCAATCATACC.	Oy 825 ATGTTGTCACAGTTTTCAGTGCCCCCAATTACTGTTACCGCTGTGGGAAC.
	125   CAAGATATTGCAGAGCAGTTCAATCATACGTTAGGTTTGCACGTGCTCACTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACTCACACCTCACCTCACACCTCACACACTCACACACTCACACACTCACACACTCACACACTCACACACTCACACACACTCA	466 AIGAAICGGTCTTTTCTTCAGTTCGAACCAGCGGCGCAANGTGAACCAGATGTGAC  964 GCGGAAGACTCCTGATTACTTTCTGTAAACATGGCCTATACATGGTACCTTTTACTTAC	Db 226 GCTCCTCTGTTCATAAAGTTGCCTTCAGAACAACTGAGATGTTGTGAATGTAACTG 167  Oy 1204 CGACAAGAGGAGCAGTGTCAATGGTTGTAAGTGATTGTGAATGTGAATGTGATGTGTGAATGTGTGTGAATG	BJ603182/c LOCUS BJ603182 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonomata Physicomitrella patens subsp. patens cDNA clone pphnlp05 3', mRNA sequence. Caulonemata and rhizoid-like protonomata Physicomitrella patens subsp. patens cDNA clone pphnlp05 3', mRNA sequence. BJ603182.1 GI:37845174 BJ703182.1

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contigs to seed DuPont contigs, this resour assembled by DuPont as part of a collaborat overgo addressing of BACs in conjunction wi Mapping Project"  Query Match 42.2%; Score 576.2; DB 4; Length 14 Best Local Similarity 75.7%; Pred. No. 5.2e-159; Matches 727; Conservative 0; Mismatches 233; Indels	210 GGTTTGGTGCCAGGGGGAGGCAGAGGTTGGGACAATGCCGTCATATGC Db 2110 GGTTTGAGGAAGCGCAGGACAAGCGGCAGGAGCGAGGACGGCAGCA	95 CGCAGAIAGAGCAGCTGTCGGAGTGCAAGCCGTTGTCGGAGTTGGAGGTTGAGGGGGGGG	0y 155 TGTGATCAAGCTCGGACGATCATGGAGGAGGAGGAGCGCT-GCAGCCCC		510 510 394 570 454		574 574 750	Oy   634 CGAGGCCGATGTGATCTACTCTGGTCTGATCCAGATGATCGTTGTG 	Db 870 TTCACCAAGGGTGCTCACATTTGCCCAAGATATTCCACAACAAT  930 AAATGGCTAAGTTTGGTTGCAGGTGCTCACCAGGTTGTGAAGGGAT  930 AAATGGCTAAGTTTGGTTGCAGGTTTTCAGTGCCCCAATTGTAATGGAAGGGT  930 AAATGGGCTAAAGTTTTCAAGAGCTCATCAACTTGTAATGGAAGGGT  930 CCAGGATAAAAATGTTGTCACAGTTTTCAGTGCCCCAATTACTTTACC  934 CCAGGATAAAAAATGTGTCACAGTTTTCAGTGCCCCCAATTACTTTTCTTC  936 CCAGGATAAGAACGTTGTGAAAAATGGCGCCCTAACTTTTCTTC  937 CATGGCCCCCATAATGGAGATAGAAGAACAGTGAAAATCGTCCTCC  934 AGCACCGCGCAAAATGAACAGAACGGAAAAATCGAACACTCTCTCC  934 AGCACCGCGCAAAATGAACAGAACGGAAAAACCTGATTACTTCTTC  1110 AGCTCCGCGGCAAATTGAACCAGAACTGACACTGATTACTTCTCTCC  934 AGCACCGCGCAAAATTGAACCAGAACTGACGGAAAACTCCTCCTCATTACTTCTTCTCTCC  934 AGCACCGCGCAAAATTGAACCAGAACTGACGGAAAACTCCTCCTCATTACTTCTTCTCTCCCTCTTTTTTTT
Db   306   CCTGAATGAAGATACTCCCTCATGATCTAGTAGTATGAAGTTATCTTTGAAGTGTTT 247	1245 ATTAGGGAAAGAAGGTAGCACATGTTACTTCAAATCGATCAGAGACTTCTATGGAAAAGA 1304 	1305 TGACGATGGTGGAAACAACGTTCATCTCCACACCTACTGTATATGGCATGCTCGAGCTCG 1364	1365 C 1365   6 C 6	AX104802 AX104802 LOCUS LOCUS AX104802 DEFINITION Zea mays PC0069597 mRNA sequence. VERSION AX104802 VERSION AX104802.1 GI:21207880 VERSION AX104802.1 GI:21207880 SOUNCE Zea mays	NISM NCE ORS	Jr. Anchoring 9,371 maize expressed sequence tagged unigenes to th bacterial artificial chromosome contig map by two-dimensional overgo hybridization Plant Physiol. 134 (4), 1317-1326 (2004)		JOURNAL Unpublished (2002)  REFERENCE 3 (beses 1 to 1429)  AUTHORS Coe, E.H.  TITLE Direct Submission  JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA	COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZnDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu, TIGR, www.tigr.org; or NCBI, www.ncbl.nlm.nih.gov. When the source of the maize CDDA sequences is either Virginia Malbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:  www.zmdb.iastate.edu.  Cocation/Qualifiers  1.1429  / organism="Zea mays"  / db_xref="WaizeGDB:633782"  / db_xref="WaizeGDB:633782"  / clone_lib="Maize Mapping Project/DuPont Cornsensus Library:  / lone="Lib="Maize Mapping Project of EST assemblies resulting from the application of public

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<pre>www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. Location/Qualifiers 1128 /organism="Arabidopsis thaliana"</pre>	8 & a	946 TACAGACCAACIATIGCIACCGGIG 901 AACAATGAATGGTCTTTTCTTCAGTTC 1006 GAACATGGGCAAAACTTCCTCCGGTTT
/plasmid="pCMVSPORT 6" complement(11283) /gene="At1g10430"	RESULT 11 CNSOAD99 LOCUS	
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GGAGGAGTGGAACCTGCAAGTGTCCTGTCACGTTTGCGGTGACATCCATGG 240 	AUTHORS TITLE	Castelli,V., Aury,J.M., Jailld Menard,M., Cruaud,C., Quetier, Temple,G., Caboche,M., Weisser Whole Genome Sequence Comparis
CAGTITCATGATCTCATCGAGCTITTCCGCATAGGAGGCAAGGCGCCCGACACGAACTA 300 	JOURNAL	A Combined Approach to Evalua Annotation Unpublished 2 (bases 1 to 1285)
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AGTGGCCCTGAAGGTGCGGTATAGGGATCACAATCTTGCGAGGGAACCACGAGAG 420 	COMMENT	- Web : www.genoscope.cns.tr) The sequences are based on sir Life Technologies (a division full-length librairies constru
CAGGCAGATTACGCAAGTATATGGTTTCTATGAATGCCTGCGGAAGTATGGAAATGC 480 		GENOSOPE MEMDERS CARTIED OUT V. JAUY J.W. Jaillon O. Wir Schachter V. Weissenbach J. VIRGY INRA : Clepet C., Cabocht
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REFERENCE AUTHORS TITLE	1 (bases 1 to 1285) Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Cler Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Sche Temple, G., Caboche, M., Weissenbach, J. and Salanoubat Whole Genome Sequence Comparisons and 'Full-Length' A Combined Approach to Evaluate and Improve Arabidor	ences:
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Matches         706;         Conservative         0;         Mismatches         225;         Indels         0;         Gaps         0;           Qy         61         GGTTGGGACAATGCCGTCATATGCAGCAGATGAGAGCTGCTGGAGTG         120           bb         166         GCTTTCAAGCTGAACCGAACTGAAGACCTAGACCAGATCGAGCAGTCTGATGAGGGCTCTTGGT         225           Qy         121         CAAGCTTTGTGGAGCTGAAGACCTTTGCGATCAGGCTTCTTGT         180           Db         226         TAAACGTTATGGAGCGGATGTGGAGCTTTTGCGATCAGGCATCCTTGT         285           Qy         181         GGAGGAGTGGAGCCGTGAAGTGTCCTGTTACCGGTTTGCGGGAACTCCTTGGGGAACTCTTCAGGGAACTCTTCAGGGAACTCTTGCGGTAACTACAGGGAACTATTCAGGGAACTATTACAGGACACCACAGAACTA         300           Db         241         CCAGTTTACATGATCCATCGAGCTTTTCGTATACGGTAACGACACGACACGAACTAACT	361 AGTEGGCCTGAAGGTGCGGTATAGGATTACAATCTTGCGAGGGAACCACGAGAG 466 GGTGGCACTAAAAGTGCGATAGGATTACAATCTTGCGAGGGAACCACGAGAG 421 CAGGCAGATTACGCATACAGGATAGATTCTACAAATCTTACGAGGGAATCACGAGAGA 421 CAGGCAGATTACGCAATATGGTTTTTATGAATGCTTGAGGAATGCAGGAATGC 481 GAATGTTTGCAAGTTCTACAGGATCTGTTCGACTGCTTGAGGAATGCTTGAGGAATGCTTGAGGAATGCTTGAGGAATGCTTGAGGAATGCTTGAGGAATGCTTGAGGAATGCTTGATTTTTACAGAGCTTTTCGATTATTCCTCTTGATATATGCTTTTTTTT	TGGACAGATATCGCAGCTCAATTTAATCACAACAATGGACTAAGTCTCATATCAAGAGC TCACCAGCTTGTGAATTTAATCACAACAATGGACTAAGTCTCATATCAAGAGC TCACCAGCTTGTGAAGGTTTAACTGGTGTCAGGATAAGAATTGTCACAGTTTT

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4.5 GATESCAMASTICATION CONTRICTANCE AND	AUTHORS  TITLE Direct Submission JOURNAL Submitted (25-APR-2002) Maize Mapping Project, Unive Missouri, Columbia, MO 65211, USA  COMMENT If you are interested in getting corresponding physithes are publicly available from ZmDB and may be for searching at MSL, maizemap.org; ZmDB, www.zmdb.iaste cDNA sequences is either Virginia Walbot. Aschable, Iowa State, then clones may be requested for www.zmdb.iastate.edu.  FEATURES  1. 1534   Organism="Zea mays"   Mol. Lype="mRNA"   Ab_xrefe="mRNA"   Ab_x	Query Match 40.8%; Score 556.6; DB 4; Length 15 Best Local Similarity 75.0%; Pred. No. 3.5e-153; Matches 722; Conservative 0; Mismatches 239; Indels Ov 37 TTTGGTGCCAGGGGGAGGGCAGAGGTTGGGACAATGCCGTCATATGCA		157 TGATCAAGCTCGGACGATCTTGGTCGAGGAGTGGAACGTGCA	1	638 . 577 698
그는 그		TCACCAGCTTGTGATGGAAGGATACAATTGGTGCCAGGATAAAAATGTTGTCACAGTTTT		gacgegaagactectgattactttetgtaa 	AY108657  AY108657  AY108657  AY108657  AY108657.1 GI:21211829  HTC.  Zea mays  I Zea mays	Plant Physiol. 134 (4), 1317-1326 (2004) 1502042 2 (bases 1 to 1534) Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design Overgo Probes Unpublished (2002) 3 (bases 1 to 1534)

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Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.
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/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
Ecory, Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-Ev. Colonies
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Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
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KEYWORDS
SOURCE
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672

732 99 792 720 780

Search completed: December 9, 2005, 09:50:43 Job time : 5152 secs

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

December Run on:

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US-10-764-259-8 1365

Title: Perfect score:

1 ggcgttaacgcgcggaggag.....tatggcatgctcgagctcgc 1365 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1303057 seqs, 888780828 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6\_COMB.seq:\*

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5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*

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8: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

9: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 8, Appli	m			10,	Sequence 17, Appl	554		9	10,	Sequence 11, Appl	٠.	269	-	N	2909	-	46,			42	4207	Sequence 38, Appl	420
SUMMARIES	D	US-09-828-302-8	US-09-780-045-3	US-09-949-016-5464	US-09-949-016-590	US-09-780-045-10	US-09-780-049-17	US-09-949-016-5543	US-09-780-049-3	US-09-300-958A-39	US-09-780-049-10	US-09-190-976B-11	US-09-828-302-3	US-09-487-558B-269	US-09-614-221A-47	US-09-487-558B-267	US-09-949-016-2909	US-09-825-497A-41	US-09-533-559-46	US-09-949-016-3862	US-09-916-338A-1	US-09-614-221A-424	US-09-248-796A-4207	US-09-300-958A-38	US-09-248-796A-4206
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Sequence 8. Application US/09828302

Patent No. 6818805

GENERAL INPORMATION:

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: CAFA E SILVA, OSWALDO DA

APPLICANT: CHEN, ROUYING

APPLICANT: ISHITANI, MANABU

TITLE OF INVENTION: PLOSPHATASE STRESS-RELATED PROTEINS AND FILE REFERENCE: 16313-0029

CURRENT FILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-08-20

PRIOR PLING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver: 2.1

SECTION OF SECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGCGTTAACGCGCGGAGGAGAGCGATCGGTTAGGGTTTGGTGCCAGGG
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; ORGANISM: Physcomitrella patens
US-09-828-302-8
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Matches 1365; Conservative
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RESULT 2   US-09-780-045-3   US-09-780-045-3   ADE   Patent No. 6602   Patent No.		0 0 0 1243 0 0 254 0 0 254 0 0 1183 0 0 0 1243 0 0 0 434	1200 Db 1363 CA 1200 Qy 494 TA 1260 Db 1423 TA 1260 Qy 554 TG 1320 Db 1483 TG 1320 Qy 614 CG Db 1543 CG
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Jacqueline Wyatt
ENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATA:
ENTION: EXPRESSION
CE: RTS-0130
ICATION NUMBER: US/09/780,045
Q ID NOS: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGTATAGGGATAGGATCACAATCTTGCGAGGGAACCACGAGAGCAG
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Pred. No. 1.2e-160;
0; Mismatches 304; Indels
oplication US/09780045
12713
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Conservative
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8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2	
1613 GATCGTGGTGGATGGATATTCACCACGTGGTGCTGGTCACACTTTTGGACAAGATT 1662  714 GCAGGCAGTCAATCAACCGAATGGTCTAAGTTTGATTGGTCACACTTTTGGACAAGATT 1662  1621 TCTAAAACCTTTAACCATCCAATGGTCTAAGTTTGATTTCACTGCCCAACTTTTGACTTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	328 CATAGRATIATIC COLOGRAGO CONTROL CO

us-10-764-259-8.rni

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rr 453 rr 265 c 513

1T 325 1C 573 3G 385 3A 633

3T 445 3C 693 1T 505 1T 753 3T 565 1T 813

iA 685

AC 805 | AT 1053

rc 745

3C 865 || 3C 1113 3C 1113 AG 925 || 173

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TTCGAACCAGCACCGCGGCAAAGTGAACCAGATGTGACGGGGAAGACTCCTGATTACTTT	698 CTTCTGTCTACATGGTGTCTCTCGCCATCTATAGATACACTGGATCATR	   757
1174 TITGACCAGCACCTCGTGGAGAGCCTCATGTGACCCGGCGCACCCAGACTACTTC 1233 986 CTGTAAA 992 	Qy 610 AGATCGTATTCAAGAAGTGCCGCACGAGGGCCCGATGTGTGATCTACTCT	3C .669
1234 CTATAAA 1240 III.T. 6	Oy 670 AGATGATCGTTGGATGGGGCATTTCACCACGAGGTGCCGGTTATACTT	3A 729 
09-780-049-17 Bequence 17, Application US/09780049 attent No. 6465250	OY 730 TAITGCAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGG	CT 789    CT 937
APPLICANT: Brett P. Monia APPLICANT: Jacqueline Wyatt TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT TITLE OF INVENTION: EXPRESSION	OY 790 TGTGATGGAAGGATACAATTGGTGCCAGGATAAAAATGTTGTCACAGTTT	CC 849  -  CC 997
FILE REFERENCE: RTS-0134 CURRENT APPLICATION NUMBER: US/09/780,049 CURRENT FILING DATE: 2001-02-09 NUMBER OF SECTED NOS: 94	OY 850 CAATTACTGTTACCGCTGGGGAACATGGCCGCATAATGGAGATAGAT	AA 909    AA 1057
LENGTH: 2181 TYPE: DNA	OY 910 TCGGTCTTTCTTCAGTTCGAACCAGCACCGCGGCAAGTGAACCAGATG	AA 969 CG 1117
AGATUS: None Saptens FRATURE: NAME/KEY: CDS LOCATION: (210)(1139)	Qy 970 GACTCCTGATTACTTTCTGTAAACATGGCCTATACATG 1007 	
National Similarity   69.1%;   Score 505.2;   DB 3;   Length 2181;	RESULT 7  US-09-949-016-5543  i Sequence 5543, Application US/09949016  j Batent No. 681239  i GENERAL INFORMATION:  i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION  CURRENT APPLICATION NUMBER: US/09/949,016  CURRENT FILING DATE: 2000-04-14  PRIOR FILING DATE: 2000-10-20  PRIOR PELING DATE: 2000-10-03  PRIOR FILING DATE: 2000-10-03  PRIOR FILING DATE: 2000-10-03  PRIOR FILING DATE: 2000-09-08  NUMBER OF SEQ ID NOS: 207012  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 5543  LENGHI: 218  TYPE: DNA  CORGANISM: Human	S THEREOF
310 GGGCGACTATGTGGATGCGTGGATATTATTCTGTCGAGACTGTGGCTCGTTAGTGGCCCT 369	OS-03-343-018-5543 Query Match 37.0%; Score 505.2; DB 3; Length 21 Best Local Similarity 69.1%; Pred. No. 3.2e-157; Matches 690; Conservative 0; Mismatches 308; Indels s	0
GAAGGTGCGGTATAGGGATAGGATCACAATCTTGCGAGGGAACCACGAGAGGGGGGCAGT 42 	10 GCGCGAGAGAGAGCCGATTAGAGTTTCGTGCCAGGGAGGAGCACGCAC	C 69
TACGCAGINTATGGTTTCTATGATGATGCTGCGGGAGTATGGAANTGCGGATGTTTG	Oy 70 AATGCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGCTCTCGGAGT 17	TT 129     CT 278
490 GARGTACTTCACGGATTCGATTACTGCCTCTGACAGCTCTCATTGAGGAGTT 549	OY 130 GTCGGAGTTGGAGGTGAACCTATGTGAAGCTCGGACGATCTTGG 	TG 189  -  C 338

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ORGANISM: Homo sapiens   SEPATURE:   NAME/KEY: CDS   NAME/KEY: CDS   SEPATURE:   SEPATUR		1363 CACACAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1603 AGATGACCGTGGTGGGTATATCTCCTCGAGGGGCTGGTTACACCT 730 TATTGCAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGCACGTG 1663 TATTTCTGAGACATTTAATCATCATGCCAATGGCCTCACGTTGGTTG
N N N N N N N N N N N N N N N N N N N	3 8 5 8 5 8 5	6 8 6 8 6 8 6	8 8 8 8 8 8 8 8
0y         190         GAACGTGCAGCCCGTGAAGTGCCCTGTCACGGTTTGCGGTGACATCCATGGCCAGTTTCA         249           0y         250         TGATCTCATGCAGTTCGATGTCGTGTGCGAGGATTTCAT         398           0y         250         TGATCTCATGGAGTTCGATGTCGTGTGCAGCACCCACCACCATTGTTCAT         309           0y         250         TGATCTCATGGAGTTTGCAGTAGGAGGAATCACCAGTACAATTACTTGTTGTTAT         458           0y         310         GGGCGACTATGTGGATATTATTCTGTCGAGATCACAATTACTTGTTGTTGTTTAT         458           0y         310         GGGCGACTATGTGGATATTATTCTGTCGAGACTGTTGTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	550 TTTTTGTCTTCATGGGGTCTCCCATCGCTCGACACATTAGGTCACCATCCGAGCCCT  [	979 INTITICIAGA MATATA CATACONA ADATOTICA CANTAGA CONTROL AND TOTAL AGAIN AND THE CONTROL AGAIN AND THE CONTRO	RESULT 8  US-09-780-049-3  Sequence 3, Application US/09780049  Sequence 3, Application US/09780049  Sequence 3, Application US/09780049  Sequence 3, Application US/09780049  PERENT NO. 6456526  APPLICANT: Brett P. Monia  APPLICANT: Brett P. Monia  APPLICANT: Brett P. Monia  TITLE OF INVENTION: ANTIENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT  TITLE OF INVENTION: EXPRESSION  FILE REFERENCE: RTS-0134  CURRENT PILING DATE: 2001-02-09  NUMBER OF SEQ ID NOS: 96  SEQ ID NO 3  LENGTH: 2966  TYPE: DA

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3A 685 3T 806 1T 866 1T 866 3C 805 3C 865 3T 986 1 1 985 1T 985 1T 985 1T 985	TALYTIC S	10 0; 10 145 10 205 11 339 11 265 10 399 11 265 10 399 11 365 12 399 12 399 13 385
	RESULT 10  US-09-780-049-10  Sequence 10, Application US/09780049  Patent No. 646220  GENERAL INFORMATION:  APPLICANT: Brett P. Monia  APPLICANT: Brett P. Monia  TITLE OF INVENTION: EXPRESSION  FILE OF INVENTION: EXPRESSION  FILE REPERENCE: RTS-0134  CURRENT APPLICATION NUMBER: US/09/780,049  CURRENT APPLICATION NUMBER: US/09/780,049  CURRENT APPLICATION NUMBER: 2001-02-09  NUMBER OF SEQ ID NOS: 96  SEQ ID NO 10  LENGTH: 1781  TYPE: DNA  ORGANISM: Mus musculus  FATURE:  NAMM-KEY: CDS  LOCATION: (196)(1125)  US-09-780-049-10	Query Match         36.1%; Score 493.2; DB 3; Length 17           Best Local Similarity         70.9%; Pred. No. 2.8e-153;           Matches 654; Conservative 0; Mismatches 268; Indels           Qy         86 GATGTAGACGGGGAGATAGAGGAGCTGGAAGCAGCTGCAGGAGGAGCTGCAAGCAGCTGCAAGCAGCTGCAAGCAGCTCTCCGAAGCAGCTGCAAGCAGCTGCAAGCAGCTGCAAGCAGCTCTCCGAAGCAGCTGCAAGCAGCTCTCCGAAGCAGCTGCAAGCAGCTGCAAGCAGCTGCAAGCAGCTGCAAGCAGCTGCAAGCAGCTGCAAGCAGCTCTCCGAAGCAGCTCTCGAAGAAGCCCTGGGAGAAGGTGCAAGAGAGCTCTGAAAAAATCCAGAAAATTCATGAACTCTGAAGAATTCATGATCT           Qy         206 AAGTGTCCTGTCACGGTTGCGGAGAATTCATGATCT           Qy         266 TTCCGCATAGGAGCACAAGAAGTACATGTTCATGAGCGAAGAATTCATGAGGGGAAGTTTATGGGGCAATTTATGGGGCAATTTATGGGGGAAGTTTATGGGGGAAGTTTATGGGGGAAGTTTATGGGGGAAGTTTATGGGGGAAGTTTATGGGGGAAGTTTATGGGGCAATTTATGGGGGAAGTTTATGGGGCAATTTATGGGGGGAAGTTTATGGGGCAATTTATGGGGCAATTTATGGGGCAATTTATGGGGCCTGAAGGTATAAATCACCAGATACAAATTACCTGTTTATGGGGCAATTTATGGGGCAATTTATGGGGCAATTTATGGGGCAATTTATGGGGGAAGTTTATGGGGCCTGAAGGTATACTTTATGTTTATGGGGCAATTTATGGGGCAATTTATGGGGCAATTTATGGGGCAATTTATGGGGCAATTTATGTTTATGGGGCAATTTATTATGGGGCAATTATTATGGGGCAATTTATTATGGGGCAATTTATTATGGGGCAATTTATTATGGGGCAATTTATTATGGGGCAATTTATTATGGGGCAATTTATTATGGGGCAATTATTATGGGGCCTGAAGGTATTATTATGGGGCAATTATTATGGGGCCTGAAGGTATTATTATGGGGCAATTATTATGGGGCCTGAAGGTATTATTATGGGGCAATATTATTATGGGGCAATTATTATGGGGCCTGAAGGTATTATATGGGGCCTGAAGGTATTATATGGGGCAATTATATTATGGGGCAATTATATTATGGGGCAATTATATTATGGGGCAATTATATTATGGGGCAATTATTATGGGGCAATTATATTATGGGGCAATTATATTATGGGGCAATTATATTATGGGGCAATTATTATGGGGCAATATGTTATATGGGGCAATTATTATATGGGGGAATATTATATGGGGCAATATGTTATATGGGGCAATATGTTATATGGGGCAATATGTTATATGTTATATGGGGCAATATGTTATATGGGGCAATATGTTATATGGGGCAATATGTTATATGGGGCAATATGTTATATGGGGCAATATGTTATATGGGCAATATGTTATATGGGCAATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATGTTATATATGTTATAT
970 GACTCCTGATTACTTTCTGTAAACATGGCCTATACATG 1007	14.44.44.44.44.44.44.44.44.44.44.44.44.4	387 TTTAGAATTGGTGGCAAATCACCAGATACAATTACTTGTTTATGGGGAGATTATGTTGC 446 326 GGTGGATATTATTCTGTGAGACTGTGGCTCTTAGTGGCCCTGAAGGTGCGGTATAGG 385 447 AGAGGATATTATTCAGTTGAAACAGTTACACTGCTTGTAGCTCTTAAGGTTCGTTACCGT 506 386 GATAGGATCACAATTCTGCGAGGAACCACGAGGCAGATATACGCT 445 507 GAACGATCACCATTCTCGAGGGAACCACGAGAGACAGATTATGGATATTATGGT 505 446 TTCTATGATGATGATCTTCTGAGGAAATGCGAATGAGAATTTTGGAAGTTTTAGGT 505 446 TTCTATGATGATGATGATGAAATGAGAATGCGAATTTTTAGGT 505 447 TTCTATGATGATGATGAAATGAGAAATGAGAATGTTTTGGAATTTTTACGAT 505 446 TTCTATGATGATGATGAAATGAGAAATGAGAAATGTTTTGGAAATTTTTACGAT 505 447 TTCTATGATGATGATGAAATGAGAAATGAGAAATGTTTTTAGAT 505 448 TTCTATGATGATGATGAAATTATGAAAATGAAATGAAAT

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ATTORNEY/AGENT INFORMATION:  NAME: David Prashker, Esq.  REGISTRATION NUMBER: 29,693  REFERENCE/DOCKET NUMBER: BIS-041  TELEPHONICATION INFORMATION:  TELEPHONE: 6789 525-3794  ORMATION FOR SEQ ID NO: 11:  SEQUENCE CHARACTERISTICS:  LENGTH: 1721 base pairs  TYPE: nucleic acid  STRANDEDNESS: single  TOPOLOGY: linear  MOLECULE TYPE: peptide  SEQUENCE DESCRIPTION: SEQ ID NO: 11:  90-976B-11	cal Similarity 68.0%; Pred. 679; Conservative 0; Mi 10 GCGCGGACGACGACGATCGGTAGA 10 GCGCGCGCGCGAGAGAGACCGGAGAGAGAGAGAGAGAGA	190 GAACGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCGGTGACATCCATGGTGTGTGCAGGTTTGCGGTGACATCCATGGTGTGTGCAGGTTTGCGGTGACATCCATGGTGTGCAGGTTTCCGCTTGTCCAGTCCTGTGCATGTGCATGTGCATGTGCATGTGCATGTGCATGTGCATGTGCATGGTGCATGTTCTGTCATGTGTGATTGTTCTGTCAAATTGTTCAAATTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTGTGAAATTGTTG	430 TACGCAAGTATATGATGAATGCCTGCGGAAGTATGGAAATG 472 CACACAAGTATATGGTTTCTACGATGATGTTTTAAGGAAATACGGAAATG 490 GAAGTATTTACAGATCTTTTGACTATCTTCCTCTCACGCCTTGTG 532 GAAGTATTTACAGACTTTTTGACTATCTTCCTCTCTCTGTGGTGG 550 TTTTGTCTTCATGGTGGTCTGTCTCCATCGTCGCTTGGTGG 550 TTTTGTCTTCATGGTGGTCTGTCTCCATCGTCGTTGGTGG 592 TTTTGTCTTCATGGTGGTCTGTCTCCATCGTCGTTGGTGG 610 AGATCTTCATGGTGGTCTTTTTGACTACTTCTCTCTTAGATCACA 610 AGATCGTTCATGGTGGTCTTCTCACCATGGTGGACTCACA 610 AGATCGTTGTGGTGGTGGTTCTCACAGGGTCCAATGTTACTCT 652 TGATGACCTTAAGAAGTTCCTCATGGGGTGCGGTTATACTT 653 TGATGACCGTGGAGGGTTTCACCATGGGTGCGGTTATACTT 710 AGATGACCGTGGAGGTTCAATCATACCATGGTGCTGTTACCTT 730 TATTGCAGAGGTTCAATCATACCATGGTCTAAGTTTGGTTACACTT 731 TATTCTGAGAAGATTCAATCATACCATGGCTCAAGTTTGGTTGCTGAGGT 772 TATTCTGAGAAGAATACATACCATGGCCCAATGGTCTAAGAGT 773 TATTCTGAGAACATTCAATCATGCCAAGATAAAAAATGTTTGGTTTAAGATTTT 774 TATTCTGAGAACATTCAATCATGCCCAAGGATAAAAAATGTTTGGTTTAAGATTTT 775 TATTTCTGAGAACATTTAATCATGCCCAAGGATAAAAAATGTTTTCTAAGATTTT 776 TGTGATGGAAGAACAATGGCCCAAGGATAAAAAATGTTTTCTAAGATTTT 777 TATTTCTGAGAACAATTGGTGCCAATGGTCTTAAGATTTT 777 TATTTCTGAGAACAATTGGTCCAAGATAAAAAAATGTTTTCTAAGATTTT 777 TATTTCTGAGAACAATGGCCCAAGGATAAAAAAATGTTTTCTAAGATTTT 777 TATTTCTGAGAACAATGGCCCAAGGATAAAAAAATGTTTTCTAAGATTTT 777 TATTTCTGAGAACAATGGCCCAAGGATAAAAAAATGTTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTCTAAGATTTTTCTAAGATTTTTCTAAGATTTTCTAAGATTTTTCTAAGATTTTTCTAAGATTTTTCTAAGATTTTTCTAAGATTTTTCTAAGATTTTTTTCTAAGATTTTTTTT
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460 AGAGGATATTACTCTGTTGAAACAGTTACACTGCTTGTAGCTCTTAAGGTTCGTTACCGA 519   386 GATAGGATCACACATCTTGCGAGGGAACCAGGAGTTACGCAAGTATATGGT 445	Qy         626 GTGCCGCACGAGGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATGATGGTTGTGGG         685           1		MESULT 11 US-09-190-976B-11 US-09-190-976B-11 Sequence 11, Application US/09190976B Sequence 11, Application US/09190976B Sequence 11, Application US/09190976B Sequence 11, Application of Application of Application of Application Stimulation of Application Data:  COMPUTER READABLE FORM:  MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC COMPUTER:

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| 4G 472
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|CA 412
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Secondary Metabolit
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	210 GTCCTGTCACGGTTTGCGGTGACATCCATGGCCAGTTTCATGAGCTTTTCC 269  329 TGCCTGTTACCATTTGTGGTGACGTACACGGTCATTTCCATGAGCTTTTTA 388  270 GCATAGGAGGCAAGGCGCCGAACACGAACTTCATGGGCGACTATGTGGATCGTG 329  270 GCATAGGAGGCAAGGCCCGAACACGAACTACTTGTTCATGGGCGACTATGTGGATCGTG 329  389 AGATTGGTGGCCCTTGTCCTGACCAATTACCTTTTCATGGGTGATTACGTGGATAGAG 448

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1049 ACCCATCCGTAAGACCAGGTGAACCTAGCGTCAGCAGAAAGACGCCCAGATTACTTTTAT 1108
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                                                                                                                                                     Query Match 29.6%; Score 404.4; DB 3; Length Best Local Similarity 65.5%; Pred. No. 8.7e-124; Matches 591; Conservative 0; Mismatches 311; Indels
                                                                                 TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-267
                  NUMBER OF SEQ ID NOS: 446
SOFTWARE: Patentin version 3.0
SEQ ID NO 267
LENGTH: 1110
PRIOR FILING DATE: 1999-10-20
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December 9, 2005, 06:30:04 Run on:

.; Search time 1078 Seconds (without alignments) 10470.966 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-764-259-8 1365 1 ggcgttaacgcgcggaggag......tatggcatgctcgagctcgc 1365

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters: 9793542 seqs, 4134689005 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications NA Main:\* Database :

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2: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:\*
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10: /cgn2 6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	1365	100.0	1365	- 6	US-09-828-302-8	Segmence 8. Appli
7	1365	100.0	1365	7	US-10-764-259-8	8
٣	596.6	43.7	1732	7	US-10-425-114-35277	
4	592	43.4	1525	8	US-10-425-115-160542	
ហ	589.6	43.2	1386	9	US-10-236-699-21	
9	584	42.8	1330	y	US-10-236-699-31	31,
7	582.8	42.7	1298	φ	US-10-236-699-25	25,
80	579.8	42.5	1195	7	US-10-437-963-40723	407
6	559.4	41.0	921	٣	US-09-938-842A-705	
10	559.4	41.0	921	m	US-09-938-842A-705	705,
11	556.6	40.8	1879	œ	US-10-425-115-149113	1491
12	552.8	40.5	1243	9	US-10-236-699-7	Sequence 7, Appli
13	547.6	40.1	1761	7	US-10-424-599-20866	
14	531.8	39.0	924	٣	US-09-938-842A-571	
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16	525.8	38.5	1484	œ	US-10-739-930-1189	Sequence 1189, Ap
17	517.4	37.9	1487	9	US-10-236-699-23	
18	515.6	37.8	2574	7	US-10-467-008-3	6
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20	514	37.7	1531	9	US-10-210-120-42	42
21	514	37.7	1531	0	US-10-909-035-42	42,
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23	512.4	37.5	1541	6	US-10-956-157-1198	1198

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US-10-388-934-575 US-09-917-800A-1625 US-10-152-319A-1641 US-10-457-008-10 US-10-467-008-10 US-09-917-800A-1624 US-10-191-803-83 US-10-388-934-574 US-10-388-934-574 US-10-388-934-574 US-10-007-926A-184 US-10-467-126-1 US-10-467-126-3 US-10-425-115-10338 US-10-425-114-32875 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-32895 US-10-425-114-35289	LIGNMENTS DA RESS-RELATED PROTE 828,302 01	imilarity 100.0%; Score 1365; DB 3; Length 12 inclarity 100.0%; Pred. No. 0; O; Indels O; Mismatches O; Indels O; Indels O; Indels O; Mismatches O; Indels O
37.4 1580 6 37.4 1843 3 37.4 1843 7 37.2 1843 7 37.2 1804 3 37.2 18004 3 37.2 18004 3 37.0 2181 6 37.0 2181 6 37.0 2181 6 37.0 2181 6 37.0 2181 6 36.7 1788 6 36.7 1789 8 36.7 1787 6 36.5 1576 7 36.5 1576 7	on US/098 502A1 ILVA, OSW LEN, NOCH UYING WYING PHOSPHATA IN PLANT IN PLANT 2001-08 000-04-07 46 er. 2.1	imilarity 100.0%; Score 1365; DB imilarity 100.0%; Pred. No. 0; Conservative 0; Mismatche 0; Mismatche 0; Mismatche 0; GGCGTTAACGCGCGGAGGAGGGGATCGGTTAGGGT GGCTTAACGCGCGGAGGAGCGGATCGGTTAGGGT GGTTGGGACATGCCGTCATATGCAGATGTAGGCT GGTTGGACATGCCGTCATATGCAGATGTAGACCGG GGTTGGGACAATGCCGTCATATGCAGATGTAGACCGG GGTTGGGACAATGCCGTCATATGCAGATGTAGACCGG CAAGCCGTTGTCGGAGTTGAAGAACCTATGT GGAGGAGTGGAACGTGCAGCCCGTCAAGT GGAGGAGTGGAACCTGCCCGTCAAGTGTCCTCTC GGAGGAGTGGAACCTGCAGCCCGTCAAGTGTCCTCTC GGAGGAGTGGAACCTGCCGTCGAAGTGTCCTCTC GGAGGAGTGGAACCTGCCCGTCGAAGTGTCCTCTC
24 5 5 10 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SULT 1 Sugar 302-8 Sequence 8, Applic Patent No. US20020 GENERAL INFORMATIC GENERAL INFORMATIC APPLICANT: COSTA APPLICANT: CHEN, APPLICANT: ISHIT TITLE OF INVENTIC TITLE OF INVENTIC TITLE OF INVENTIC CURRENT APPLICATION PRIOR APPLICATION PRIOR FILING DATE SOFTWARE: PATENTING DATE NUMBER OF SEQ ID SOFTWARE: PATENTING DATE NUMBER OF SEQ ID SOFTWARE: PATENTING DATE SOFTWA	Ouery Match Best Local Similarity Matches 1365; Conser    GCGTTAAC   GCGTTAAC   GCGTTAAC   GCGTTAAC   GCGTTAAC   GCGTTAAC   GCGTTAAC
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GTCTGATCCAGATG TGGTCAAGATATG TGGTCAAGATATTG TGGTCAAGATATTG TCACCAGCTTGTGA TCACCAGCTTGTGA TCACCAGCTTGTGA	CCCCAATT				SSULT 3 5-10-425-114-35277 Sequence 35277, Application US/10425114 Bublication No. US20040034888A1 GENERAL INFORMATION: APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua APPLICANT: Soreen, Steven E APPLICANT: Soreen, Steven E APPLICANT: Tabaska, Jack B APPLICANT: Soreen, Steven E APPLICANT: Tabaska, Jack B APPLICANT: Soreen E APPLICANT: Tabaska, Jack B APPLICANT: Tabaska,	
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                          GACTATGTGGATCGTGGATATTAT
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QY         695 TCACCACGAGGTGCCGGTTATACTTTTTGGTCAAGATATTGCAGAGCAGTT.           Db         870 TCACCAAGAGGTGCTGGATACACATTTTGGTCAAGATATTGCACAACAATT.           QY         755 AATGGTCTAAGTTTGGTTGCACGTGCTCACCAGCTTGTGATGGAAGGATA.           Db         930 AATGGGCTAAGTTTGCACGTGCTCACCAGCTTGTAATGGAAGGATT.           QY         815 CAGGATAAAAATGTTGTCACAGTGCTCATCAACTTGTAATGGAAGGGTT.           QY         815 CAGGATAAAAAATGTTGTCACAGTTTTCAGTGCCCCCAATTACTGTTACCG.           Db         990 CAGGATAAAAAAGTTGTGACAGTGTTCAGCGCGCCTAACTTACTACCG.           QY         875 ATGGCGCCCCATAATGGAAGATACTATTCTACAGG		; PUBLICATION NO. US20030150028A1 ; GENERAL INFORMATION ; APPLICANT: BOHNERT, HANS J. ; APPLICANT: CHEN, RUCYING ; APPLICANT: ISHTANI, MANABA ; APPLICANT: VAN THELEN, NOCHA ; APPLICANT: OSTA E SILVA, OSWALDO DA ; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPE ; TITLE OF INVENTION: METHODS OF USE IN PLANTS ; TILE OF INVENTION: METHODS ; CURRENT APPLICATION NUMBER: US/10/236,699 ; CURRENT FILING DATE: 2002-09-05	S -S	Query Match Best Local Similarity 75.4%; Score 589.6; DB 6; Length 13 Best Local Similarity 75.4%; Pred. No. 4.7e-179; Matches 733; Conservative 0; Mismatches 239; Indels Qy 20 GAGGGATGGGTTAGGGTTTGGTGCCAGGGGGAGGCAGAGGTGGGAC Db	101 140 140 161 200	DD   221 CGGGTTAAGTGCCCGGTCACGGCGACGATATTCACGGCCGGTCTAAGTCCGGTCAGTTCTAAGTCGCGACGGTCAGTTCAAGTCGCGACGGTCAGTTCAAGTCGACGGCCGACGACGTCATTCTTCATCAGTCGACGACGCCCGAATTATCTCTTCATCAGTCGACTGTCAGTCGCCTTAGTGGCCCTTAGTGGCCCTTAGTGGTCGTTAAGTGGGCCTTAGTGGTCAGTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGCCTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGCTTTAAGTGGGGGCTTTAAGTGGGGGCTTTAAGTGGGGGCTTTAAGTGGGGGCTTTAAGTGGGGGCTTAAGTGGGGCTTTAAGTGGGGGCTTTAAGTGGGGGCTTTAAGTGGGGGCTTTAAGTGGGGGCTTAAGTGGGGGCTTTAAGTGGGGGCTTTAAGTGGGGGCTTAAGTGGGGGCTTAAGTGGGGGGGG
Sequence 160542, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(53222)B CURRENT APPLICANTION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326	; SEQ ID NO 160542 ; LENGTH: 1525 ; TYPE: DNA ; ORGANISM: Zea mays ; FEATURE: ; LCCATION: (1)(1525) ; OTHER INFORMATION: unsure at all n locations ; FEATURE: ; OTHER INFORMATION: Clone ID: MRT4577_77994C.1 US-10-425-115-160542	Query Match         43.4%;         Score 592;         DB 8;         Length 1525;           Best Local Similarity 76.0%;         Pred. No. 8.38-180;         Agps 0;           Matches 730;         Conservative 0;         Mismatches 230;         Indels 0;         Gaps 0;           Qy         35 GGTTTGGTGCAGGGGAGGGCAGAGGTTGGACATGCCGTATGTAGACAGAGAGAG	155 TGTGATCAAGCTCGGACGACGAGGAAGTGGAACGTGCAAGTGCTCTTGTGCTGAAGTGTCCTTGTGGAAGTGTCCTTGTGGAAGTGTCCTTGTGGAAGTGCTCTTGTGTGGAAGTGTCCTTGTGTGGAAGTGTCCTTGTGTGGAAGTGTCCTTGTGCGTGC		Db 570 ACATATTGAGGAAATGAGGAAATAACTCAAGGTTGTTCTATGAT 629  Qy 455 GAATGCCTGCGAAATAGGAAATGCTAATGAAGTACTCAAGGATCTTCTATGAT 629  Qy 630 GAATGCTTGCGGAAATGCAAATGCTAAGTATTTTGAAGTACTTACAGATCTGTTGAC 514  Db 630 GAATGCTTGCGGAAATGCAAATGCTGGGAAGTACTTTACAGACTTGTTGAT 689  Qy 515 TACCTGCCTCTGACAGCTCTCATTGAGCAGATTTTTTTGTCTTCATGGTGTCTGTC	Oy         575 CCATCGCTCGACATTAGATCACATCCGAGCCCTAGATCGTATTCAAGAAGTGCCGCAC 634           Db         750 CCATCACTGCATACTTTGGATAATGTCCGCTCCTTGATCGCATACAAGAGGTCCCGCAT 809           Qy         635 GAGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGTGGAGGGCATT 694           Db         810 GAAGGACCTATGTGTGATCTTTTTTTTTGTGGTCTGACCCGGATGACAGTGGGGAATT 869

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										TACTTTCTGTAA 991                   TATTTTTGTAA 1012	SULT 6 Squence 31, Application US/10236699 Squence 31, Application US/10236699 Publication No. US20030150028A1 GENERAL INFORMATION: APPLICANT: BOHBERT, HANS J. APPLICANT: BOHBERT, HANS J. APPLICANT: SHITANI, MANABU APPLICANT: THEN FROYING APPLICANT: OSTA E SILVA, OSWALDO DA TITLE OF INVENTION: METHODS OF USE IN FILE REFERENCE: 16313-0161 CURRENT APPLICATION NUMBER: 00/10/236,65 FRICE REFERENCE: 16313-0161 CURRENT FILING DATE: 2002-09-05 PRIOR PRIOR PLING DATE: 2001-09-05 NUMBER OF SEQ ID NOS: 43 SSG ID NO 31 LENGTH: 1330 TYPE: DNA ORGANISM: Oryza sativa
Qy 380 Db 401	Oy 440		Oy 560 Db 581	Oy 620 Db 641	Qy 680 Db 701	Qy 740 Db 761	Oy 800 Db 821	Oy 860 Db 881	Oy 920 Db 941	Qy 980 Db 1001	RESULT 6  US-10-236-699-31  Sequence 31, Applicat  Publication No. US200  GENERAL INFORMATION:  APPLICANT: GHEN, RU  APPLICANT: GHEN, RU  APPLICANT: GHEN, RU  APPLICANT: CHEN, RU  APPLICANT: CSTANI  APPLICANT: CSTANI  APPLICANT: CSTANI  TITLE OF INVENTION:  TITLE OF INVENTION:  TITLE OF INVENTION:  TITLE OF INVENTION:  FILE REFERENCE: 1631  CURRENT FILING DATE:  PRIOR APPLICATION NU  PRIOR APPLICATION NU  PRIOR APPLICATION NU  PRIOR APPLICATION NU  SEQ ID NO 31  LENGTH: 1330  TYPE: DNA  CORGANISM: OYZA SAT  US-10-236-699-31

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US-10-236-699-25; Application US/10236699; Sequence 25, Application US/10236699; Publication No. US20030150028A1; PUBLICANT: BOHNERT, HANS J.

42.8%; Score 584; DB 6; Length 1330; 76.2%; Pred. No. 2.9e-177;

Query Match Best Local Similarity

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Db   879   CAAGGGCACATCGTAATGGAAGCATTTAATTGGTGTCAGGACAAG,	RESULT 8  US-10-437-963-40723  US-10-437-963-40723  Sequence 40733, Application US/10437963  Publication No. US20040123343A1  SEQUENCE 40735, Application US/10437963  Publication No. US20040123343A1  APPLICANT: La Rosa, Thomas J.  APPLICANT: Lao, Yinua  APPLICANT: Cao, Yongwei  APPLICANT: Boukharov, Andrey A.  APPLICANT: Burbazuk, Brad  APPLICANT: Li, Ping  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molititle OF INVENTION: Rice Nucleic Acid Molecules and Other Molititle OF INVENTION: Rice Nucleic Acid Molecules and Other Molititle OF INVENTION: Rice Nucleic Acid Molecules  TITLE OF INVENTION: Rice Nucleic Acid Molecules  CURRENT APPLICANT: 2003-05-14  CURRENT APPLICANT: 2003-05-14  NUMBER OF SEQ ID NOS: 204966  SEQ ID NO 40723  IENGTH: 1195  TYPE: DNA  CORGANISM: Oryza sativa  FEATURE:  COTHER INFORMATION: Clone ID: PAT_MRT4530_44137C.1  US-10-437-963-40723	Query Match Best Local Similarity 76.9%; Pred. No. 6.38-176; Matches 707; Conservative 0; Mismatches 212; Indels  Oy 73 GCCGTCATATGCAGATGTAGACCGCAGATAGAGCAGTGCAGAGTGCAGAGAGTGCAGAGAGCAGTGCAGAGTGCAGAGAGTGCAGAGAGTGCAGCAGTGCAGAGGCCATAGAGAGCCAGAGAGGCCATAGAGAGCCAGAGAGCCATAGAGAGCCAGAGAGCATACAGGAGCCAAGAGCCAACATACAGGAGCCAAGAGCCCAACAGTGCAGAGCCCAACAGTGCAGAGCCCCAACAGTGCAGAGCCCCAACAGAGGCCAACACACAAGAGACCCCAACACAACA
APPLICANT: CHEN, RUOYING APPLICANT: ISHITANI, MANABU APPLICANT: ISHITANI, MANABU APPLICANT: VAN THIELEN, NOCHA APPLICANT: COSTA E SILVA, OSWALDO DA TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND TITLE OF INVENTION: METHODS OF USE IN PLANTS FILE REFERENCE: 16313-0161 CURRENT APPLICATION NUMBER: US/10/236,699 CURRENT APPLICATION NUMBER: 60/317,305 PRIOR APPLICATION NUMBER: 60/317,305 PRIOR PILING DATE: 2001-09-05 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver: 2.1 SEQ ID NO 25 LENGTH: 1298	Mail	0

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Db 781 AACTACTGTTACAGATGTGGAAACATGGCCGCAATTCTTGAGATTGGAGA  Qy 911 CGGTCTTTCTTCAGTTCGACCAGCGCGCAAAGTGAACCAGATGT	40		CURRENT APPLICATION NUMBER: US/10/425,115 ; CURRENT FILING DATE: 2003-04-28 ; NUMBER OF SEQ ID NOS: 369326		; FEATURE: ; OTHER INFORMATION: Clone ID: MRT4577_67515C.1 US-10-425-115-149113	Query Match 40.8%; Score 556.6; DB 8; Length 18 Best Local Similarity 75.0%; Pred. No. 2.7e-168; Matches 722; Conservative 0; Mismatches 239; Indels	OY 37 TTTGGTGCCAGGGGGGGGGGGGGGGGGTTGGGACAATGCCGTCATATGCAG.	OY 97 GCAGATAGAGCAGCTGTCGGAAGTGCAAGCCGTTGTCGGAGTTGGAGGTGA.	Db 278 CGAGCCGAAGGCCTTCTTGGTGGAGGAGGAACGTGCAGCCCGTGA.	Qy 21.7 CACGGTTTGCGGTGACATCCATGGCCAGTTTCATGATCTCATCGAGGTTTT	Oy 277 AGGCAAGGCGCCGACACGAACTTGTTCATGGGCGACTATGTGGATC	Oy 337 TTCTGTCGAGACTGTCGCTCTTAGTGGCCCTGAAGGTGCGGTATAGGG.	Oy 397 AATCTTGCGAGGGAACCACGAGGGAGCAGGTATACGCAAGTATATGGTT"	OY 457 ATGCCTGCGGAAGTATGGAAATGCGAATGTTGGAAGTACTTCACGGATC"	Qy 517 CCTGCCTCTGACAGCTCTCATTGAGCACGAGATTTTTTGTCTTCATGGTG 
CURRENT APPLICATION NUMBER: US/09/938,842A  CURRENT FILING DATE: 2001-08-24  PRIOR FILING DATE: 2000-08-24  PRIOR FILING DATE: 2000-08-24  PRIOR FILING DATE: 2000-08-24  PRIOR FILING DATE: 2001-01-16  PRIOR PLING DATE: 2001-06-22  PRIOR PLING DATE: 2001-06-22  NUMBER OF SEQ ID NOS: 5379  SEQ ID NO 705  LENGTH: 921  TYPE: DNA  ORGANISM: Arabidopsis thaliana US-09-938-842A-705	Query Match Best Local Similarity 75.5%; Pred. No. 2.1e-169; Matches 695; Conservative 0; Mismatches 226; Indels 0; Gaps 0;	71 ATGCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGCTGCTCGGAGTGCAAGCCGTTG 130 	131 TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGGACGATGGTGTGGAGGAGGGGTGG 190	191 AACGTGCAGCCGTGAAGTGTCCTGTCACGGTTTGCGGTGACATCCATGGCCAGTTTCAT 250	251 GATCTCATCGAGCTTTTCCGCATAGGAGGCAAGGCGCCCGACACGAACTACTTGTTCATG 310	GACCIANTIONS INTERCEPT OF THE CONTROLL OF T	AGGRANTITION AND THE TOTAL OF T	ACGCAAGTATATGGTTTCTATGATGATGCCTGCGAAGGAATGCATGAAATGCGAATGTTTGG	AAGTACTTCACGGGTTTTGACGAAGCCTCGACAGCTCTCAAAGCACAGAGTTTCACACAGATTTTAAACAGCTCTCTCAAAGCTTTCATTAAACAGAAGATTTTTAAAAAAAA	TITIGICITANGGIGGICTICANGGICGACACATAGATCACAGCCCTA	GATCGTATTCAAGAAGTGCCGCACGAGGGCCCGATGTGTGTG	GATGATCGTTGTGGATGGGGCATTTCACCACGAGGTGCCGGTTATACTTTTGGTCAAGAT	601 GACGATCGTTGTGGATGGGGGATATCTCCTCGTGGTGGTTGCTGTTTGGACAGGAC 660 731 ATTGCAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGCACGTGCTCACCAGCTT 790	GTGATGGAAGGATACAATTGGTGCCAGGATAAAAATGTTGTCACAGTTTTCAGTGCCCCCCCC	721 GTANIGGANGGCINTAATTGGIGTCAGGANAAGANCGINGIGACAGIGITTAGIGCACCG 780 851 AATTACTGTTACCGCTGTGGGAACATGGCCGCATAATGGAGATAGAT

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                FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(1761)
OTHER INFORMATION: unsure at all n locations
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FEATURE:
1. OTHER INFORMATION: Clone ID: PAT_MRT3847_118848C.1
US-10-424-599-20866
ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                  Sequence 511, Application US/09938842A

Batent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR PLING DATE: 2000-08-24
PRIOR PLLING DATE: 2000-08-24
PRIOR PLLING DATE: 2000-08-24
PRIOR PLLING DATE: 2001-01-16
PRIOR PLLING DATE: 2001-01-16
PRIOR PLLING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 571
LENGTH: 224
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39.0%; Score 531.8; DB 3;
Best Local Similarity 73.7%; Pred. No. 1.8e-160;
Matches 677; Conservative 0; Mismatches 242;
                                                 964 GCGGAAGACTCCTGATTACTTTCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-571
                                                                                                                                                                                                             RESULT 14
US-09-938-842A-571
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W 372

NA 492

T 552 || |T 485

3A 612 || 3A 545

3A 672 || 3A 605

VT 732 || \T 665

17 792 |-| 725

NA 852

3G 912 A 845 

Db 186 TCTAATCGAGCTTTTTCGTATCGGTGGTTCTTCTCCTGATACTAATTATC  Qy 313 CGACTATGTGGATGTGGATATTATTCTGTCGAGACTGTGGCTCTTAG  Db 246 TGATTATTCTTCTGTCGAGACTGTTCTTTAGTTCTTTAGTTCTTTAGTTCTTTAGTTCTTTAGTTCTTTAGTTCTTTAGTTCTTTAGTTCTTTAGTTCTTAGTTCTTAGTTCTTAGTTCTTAGTTCTTAGTTCTTTAGTTCTTAGTTAG	373	OY 433 GCAAGTATATGGTTTCTATGAAGGCTGCGGGAAGTATGGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGGTTTTATGATGAATGTTTGAGGAAATATGGAAATGCAAAGCCTGCGGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGCTAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCAGAAATGCGAAATGCGAAATGCGCTAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCGAAATGCAAATGCGAAATGCAAATGCGAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAATGCAAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAAATGCAAAATGCAAAATGCAAAATGCAAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAAATGCAAAAATGCAAAAATGCAAAAATGCAAAAAATGCAA	OY 493 GTACTTCACGGATCTCTTCGACTACCTGCCTCTGACACTCTCATTGAGC	Oy 553 TIGICITCATGGTGTCTCCCATCGCTCGACACATIAGATCACATC	OY 613 TCGTATTCAAGAAGTGCCGCACGAGGGCCCGATGTGTGATCTACTCTGG3	QY         673 TGATCGTTGTGGATGGGGCATTTCACCACGAGGTGCCGGTTATACTTTTC           DD         606 TGACCGATGCGGTTGGGGAATATCTCCTCGTGGTGCAGGCTACACTTTCC	Oy 733 TGCAGAGCAGTTCAATCAATGGTCTAAGTTTGGTTGCACGTGCTTGTTGCTTGC	Qy 793 Db 726	Qy 853	913 GTCTTTCTTCAGTTCGAACCAGCACGGGCAAAGTGAACCAGATGTAA 	Oy 973 TCCTGATTACTTTCTGTAA 991 	Search completed: December 9, 2005, 10:13:43 Job time : 1081 secs					
	TGACCGATGCGGTTGGGGAATATCTCCTCGTGGTGCAGGCTACATTTCGGACAGATAT TGCAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGCACGTGCTCACCAGGTTGT TGCAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGCACGTGCTCACCAGGTTGT	806 GECIACICAGITIAACCACACAANGGACICICICIGATITICAAGAGCACATCAACTIGT 725 793 GAIGGAAGGAIACAATIGGIGCCAGGAIAAAAATGTIGICACAGTITICAGIGCCCCCAA 852	TTACTGTTACCGCTGTGGGAACATGGCGCCGTTATGGAGATAGAT	GTCTTTCTTCAGTTCCAACCACCCCGCAAAGTCAACCAGATGTGACGCGGAAAGTCTTTCTT	TCTGATTACTTTCTGTAA 991		pli US2 ION		TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TILLS OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIF1300-3 CURRENT APPLICATION NUMBER: US/09/938,842A	CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647	PRIOR FILING DATE: 2001-01-16 PRIOR PELING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379 EQ ID NO 571	LENGTH: 924 TYPE: DNA ORGANISM: Arabidopsis thaliana -09-938-842A-571	Query Match Best Local Similarity 73.7%; Pred. No. 1.8e-160; Matches 677; Conservative 0; Mismatches 242; Indels 0; Gaps 0;	73 GCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGCTGTCGAGCCGTTGTC 132 	133 GGAGTIGGAGGIGAAGAACCTATGIGATCAAGCTCGGACGATCTTGGTGGAGGAGGGGA 192 	193 CGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCGGTGACATCCATGGCCAGTTTCATGA 252 	

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## November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_Main) and .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published Applications AA Main) and .rapbm (Published Applications AA New).

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5, Appli
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49333, A
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Sequence 37665, A
Sequence 62270, A
                                                                     9, 2005, 07:11:40 ; Search time 242 Seconds (without alignments) 2108.725 Million cell updates/sec
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44636,
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9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq3:*
Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-750-185-37665
US-10-750-185-62270
US-11-074-176-361
US-11-074-176-361
US-11-075-185-6345
US-10-750-185-6345
US-11-121-086-52
US-10-750-185-3638
US-10-750-185-3688
US-10-750-185-46888
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US-10-750-185-835
US-10-750-185-44636
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US-10-750-185-55420
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      3392430 segs, 186927314 residues
                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA New:*
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Maximum Match 100%
Listing first 45 summaries
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	28	ä	٠	173602	7	1-121-086-2	Sedi	Appl
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υ	30	31.4	٠	963	9		Sedi	, Ap
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υ	32	31.4	2.3	1082144	7	US-11-117-187-211	Sec	. Ap
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υ	34	31		1685			Sedr	17, A
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PILLING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 37665
LENGTH: 1964
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US-10-750-185-37665
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     Sequence 62270, Application US/10750185

Sequence 62270, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MI GENOMICS, INC.

APPLICANT: KERR, Richard

APPLICANT: KERR, Richard

APPLICANT: RATES, Stephen

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31
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2.7%; Score 36.6; DB

Best Local Similarity 65.1%; Pred. No. 0.13;

Matches 54; Conservative 0; Mismatches
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GENERAL INFORMATION: APPLICANT: Klaenhammer, Todd R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bovine 19866880123096
US-10-750-185-62270
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 62270
US-10-750-185-62270
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Sequence 37665, Application US/10750185

Sequence 37665, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: KERN, Richard

APPLICANT: ROSENPELD, David

HOLM, Tom BATES, Stephen

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; LOCATION: (0)...(0); OTHER INFORMATION: ORF 1201; GTP-binding protein Bra
US-11-074-176-253
                             NAME/KEY: misc feature
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               APPLICANT: Alternan, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
APPLICANT: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR PILING DATE: 2005-03-07
PRIOR PILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: Altermann, Eric
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT APPLICATION NUMBER: 60/551,161
PRIOR PELING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: PESTSEQ for Windows Version 4.0
SEQ ID NO 253
LENGTH: 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

; IJCGATION: (0)...(0)

; OTHER INCEMATION: ORF 1201; GTP-binding protein Era

US-11-074-176-361
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Lactobacillus acidophilus
FRATURE:
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Publication No. US20050250135Al
GENERAL INFORMATION:
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ORGANISM: Lactobacillus acidophilus
Russell, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (1)...(903)
FEATURE:
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LOCATION: (1)...(924)
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                                                                                                                                                                                                     947 AGTGAACCAGATGTGACGCGGAAGACTCCTGATTACTTTCTGTAAACATC
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Score 36; DB 7; Length 924;
Pred. No. 0.13;
0; Mismatches 110; Indels
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Publication No. US20050261223A1

GENERAL INFORMATION:
APPLICANT: Czech, Michael P.
APPLICANT: Powelka, Aimee
APPLICANT: Guilherme, Adilson L.
APPLICANT: Cherniack, Andrew D.
TITLE REFERENCE: 17738-009001
CURRENT APPLICATION NUMBER: US/11/075,646
CURRENT PILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/550,677
PRIOR PILING DATE: 2004-03-05
NUMBER: OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 7292
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APPLICANT: MMI GENOMICS, INC.
  Query Match
Best Local Similarity 48.1%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2944 AAATGGATTTTC 2933
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Matches 71; Conservative
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ORGANISM: Homo sapiens
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US-11-121-086-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1087 TGATCTAGTAGTATGAAGTTATCTTTTGAAGTGTTTGTTCCCTTTTTTAGTACTTGCT
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Sequence 18, Application US/11121086
Sequence 18, Application US/11121086
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR RIPLING DATE: 2004-05-04
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                                                        APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: UNMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ DI NOS: 64922
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 63345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 7; Length 175023; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2569;
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43.9%; Pred. No. 22;
**ive 0; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.5%; Score 34.2; DB 6; Length 2 Best Local Similarity 64.6%; Pred. No. 1.1; Matches 51; Conservative 0; Mismatches 28; Indels
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; ORGANISM: Bovine 19866880467000
US-10-750-185-63345
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SOFWARE: Patentin version 3.3
SEQ ID NO 188
LENGTH: 175023
DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 43.9
Matches 145; Conservative
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CORGANISM: Homo sapiens
US-11-121-086-18
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APPLICANT: DeNISE, Sue K.
APPLICANT: ENGRER, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: COMPOSITIONS FOR INFERRING BOVINE TRAITS
ITILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT PELLING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
FRIOR PAPLICATION NUMBER: US 60/437,482
SOFTWARE: PARENCE: MOUNT OF SEQ ID NOS: 64922
SOFTWARE: PARENTIN VERSION 3.1
SEQ ID NO 3553
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALY
FILE REFERENCE: 09138.6000-000000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
                                  2.5%; Score 33.8; DB 7; Length 166
58.4%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        805 CAATTGGTGCCAGGATAAAATGTTGTCACAGTTTTCAGTGCCCCCAATT
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1141 CTTGCTCCTCTGTTCATTCATAAGTTGCCTTCAGAACAACTGAGATGTT
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                                                                                                                                                                100287 TriccrargacargeGreraccaararrig 100316
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                                                                                                            1201 CTGCGACAGAGGAGCAGTGTCAATGGTTG
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Publication No. US20050260603A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              Sequence 52, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
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Best Local Similarity 58.4<sup>§</sup>
Matches 59; Conservative
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ORGANISM: Homo sapiens
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US-10-750-185-3553/c
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TYPE: DNA
CORGANISM: Homo sapiens
US-11-121-086-100
LENGTH: 124972
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US-11-121-086-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1186 ATGTTGTGAATGTAACTGCGACAAGAGGAGCAGTGTCAATGGTTGCAAGGGTTATAGTGA 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  986 AGAATGTTAAAGAAAATACTAGATGATTCAAAGATAGACTTTTGGTTAAGCTCATACAGA 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1246 TTAGGGAAAGAAGTAGCACATGTTACTTCAAATCGATCAGAGACTTCTATGGAAAAGAT 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1046 AAAGTTCCATAAATCAGCTCAACTAAACAAATATATCTTAAAAAATTAAAGGAAGAGAT 1105
                                                                                                                                                                          431 CAACCATGAATGCAGACACCTTACTGAATATTTTACCTTTAAGCAGGAAT-----GTGA 378
                                                                   491 İGİCTIATATİTATGGGIÇCIGAAĞAİTCIĞİAİCCAAĞIACATİATTICİTCIĞAĞAĞĞ 432
                                                                                                                          GAACCACGAGAGCAGGAGATTACGCAAGTATATGGTTTCTATGATGAATGCCTGCGGAA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           926 TGCAGTGTTCTTTCAGTGTCTAAAATGTGCACATTTAAAGTCCCCTTGGCCCAATATTAT 985
                      TGTGTCGCTCTTAGTGGCCCCTGAAGGTGCGGTATAGGGATAGGATCACAATCTTGCGAGG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT FILING DATE: 2005-05-04
PRIOR PILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
SOFTWARE: PALCHING DATE: 2004-05-04
SOFTWARE: PALCHING DATE: 2004-05-04
SOFTWARE: PALCHING DATE: 2004-05-04
SOFTWARE: PALCHING VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Publication No. US20050260603A1

GENERAL INPORMATION:

APPLICANT: WHI GENOUICS, INC.

APPLICANT: BANISE, Sue K.

APPLICANT: ROSENFEN, Bachard

APPLICANT: ROSENFEN, David

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: FANTIN, Demnis

TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PatentIIN Version 3.1

LENGTH: 3156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32.8; DB 6; Length 3156;
Pred. No. 3.6;
0; Mismatches 92; Indels 0
                                                                                                                                                                                                                               469 GTATGGAAATGCGAATGTTTGGAAGTACTTCACGGATCTGTTCGACT 515
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Publication No. US20050266459A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Bovine 19866881216971
US-10-750-185-46888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.4%;
Best Local Similarity 48.9%;
Matches 88; Conservative
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ORGANISM:
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3G 23874
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                                                                                                                                                                                                                                                                    Sequence 99, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: WUCLEIC ACID PROBES AND NUCLEIC ACID ANAI
TITLE OF INVENTION: WUCLEIC ACID PROBES AND NUCLEIC ACID ANAI
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR PELICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOUTHAND: PALCHIIN VERSION 3.3
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APPLICANT: Wen, Tsui-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration
TITLE OF INVENTION: Materials and Methods for the Alteration
TITLE OF INVENTION: Accept CoA Levels in Plants
FILE REFERENCE: P2194USDIV-2
CURRENT EPLINGNION NUMBER: US,11/167,856
CURRENT FILING DATE: 2005-06-27
PRIOR PILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 99/344,882
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-35
NUMBER OF FILING DATE: 1998-06-35
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VET: 3.1
DB 7; Length 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4%; Score 32.8; DB 7; Length 134 71.7%; Pred. No. 46;
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                                                                                                   IGCTCCTCTGTTCATTCATAAAGTTGCCTTC
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                                                17; Indels
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Score 32.8; DB
Pred. No. 44;
0; Mismatches
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APPLICANT: Nikolau, Basil J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wurtele, Eve S
Oliver, David J
Behal, Robert
Schnable, Patrick S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ke, Jinshan
Johnson, Jerry L
Allred, Carolyn C
Fatland, Beth
                                                                                                   1124 TGTTCCCTTTTTAGTACT
Query Match
Best Local Similarity 71.7%;
Matches 43; Conservative
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1237 ccaaagartrcarcrrggrararcrrcararccrcagrgacarcrgggaarararggr 1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  813 GCCAGGATAAAATGTTGTCACAGTTTTCAGTGCCCCCCAATTACTGTTACCGCTGTGGGA 872
                                                                                                                                                                                                                                                     753 CCAATGGTCTAAGTTTGGTTGCACGTGCTCACCAGCTTGTGATGGAAGGATACAATTGGT 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1117 TITITACCGIGCTCAAIGIAAGAIAGAATCTICICAAACTGICTITATCCACTT 1063
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; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: POLIM, Tom
; APPLICANT: POLIM, Tom
; APPLICANT: POLING NOWNER: US/10/750,185
; TILE REPERENCE: MMI1100-2
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; LEWITH OF SEQ ID NOS: 64922
; SOFTWARE: PATENTING TOWNER OF SEQ ID NOS: 64922
                                                                                                                                             Query Match 2.4%; Score 32.6; DB 7; Length 1614; Best Local Similarity 49.1%; Pred. No. 2.6; Matches 86; Conservative 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.4%; Score 32.6; DB 6; Length 1721; Best Local Similarity 50.3%; Pred. No. 2.8; Matches 80; Conservative 0; Mismatches 79; Indels 0
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; ORGANISM: Bovine 19866880961460
US-10-750-185-62692
; SEQ ID NO 21
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Arabidopsis Thaliana
US-11-167-856-21
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US-10-750-185-62692
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version	sw model	08:23:56 ; {w 98	жрг	. 0.5	18781 residues	chosen parameter		% summaries	* *	sults o the the t	SUMMARIES		B77578	IP98034 IP98039	G31595	Y24822	G40766	G32348	G29592	G31596	G32349	G67626	G67447	AAE33198 ADE85518
GenCore (c) 1993	sing	005,	13 QLSEC	Gapext	43937		000	0 <b>%</b> 100 45	Geneseq_21:* geneseqp1990s:* geneseqp2000s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003s:* geneseqp2003bs:* geneseqp2004s:*	of regions of		OI S	i											
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	OM protein	Run on:	Title: Perfect Sequenc	Scoring	Searched	Total n	Minimum Maximum	Post-pr	Databas	டி <b>ம</b> π்		Result No.	1 7 7 7	w 4	o o	. r a	9 6	110	13	15	17	100	212	233

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Adc16	Ade	Ade	Add	Add	Adl	Adx	Ady	Ady	Aao	Aao	App	Aae	Aae	Adbe	Adc	Adje	Ads	Adx	Ady	Abp
ADC16730	ADE63503	ADE63505	ADD45927	ADD45925	ADL83148	ADX05674	ADY70515	ADY97844	AA022786	AA022787	ABB57104	AAE33199	AAE33200	ADB85517	ADC16729	ADJ66518	ADS88193	ADX08187	ADY70516	ABP98035
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85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.3
1427	1427	1427	1427	1427	1427	1427	1427	1427	1411	1411	1411	1411	1411	1411	1411	1411	1411	1411	1411	1408
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## ALIGNMENTS

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AC ABB77578;		
or 02-SEP-2002 (first entry)		
DE Physcomitrella patens PP2A-4 SEQ ID NO 13.		
AA Physcomitrella patens; PHSRP; phosphatase stress related XW PP2C; enzyme; transgenic; plant; stress tolerance.	pr	'P2A;
AA OS Physcomitrella patens.		
XX PN WO200246442-A2.		
XX PD 13-JUN-2002.		
XX PF 06-APR-2001; 2001WO-US011253.		
XX PR 07-APR-2000; 2000US-0196001P.		
XX PA (BADI ) BASF PLANT SCI GMBH.		
Da Costa E SilvaO, Bohnert HJ, Ishitani M,	Van Thielen N	ж ;
XX DR WPI; 2002-508562/54. DR N-PSDB; ABN81332.		
XX Property of the contransformed by phosphatase stress properin coding nucleic acid whose expression in the cell refer increased tolerance to environmental stress compared to wil		e11.
XX PS Claim 16; Fig 3; 106pp; English.		
The invention relates to a transgenic plant cell	(I) transf	æ
phosphatase stress-related protein (PHSRP)	•	81330-
CC ABN81334), where expression of the nucleic acid in the plan		esulta
type variety of the plant cell. PHSRP encod	us	
		for
		ated
-		s of
CC interest, evolutionary studies, determination of PHSRP regi		ired
cc for immediation, modulation of a fusic activity, modulation of		4

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transport of one or more compounds and modulation of stress resistance. The gene is also useful for identifying and/or cloning PHSRP homologues in other cell types and organisms, for identifying an organism as being P. patens or its close relative and for evolutionary and protein	TY YY	
structural studies. The present sequence is that of a FhSkF of the invention Sequence 306 AA;		The invention re
Query Match 100.0%; Score 1670; DB 5; Length 306; Best Local Similarity 100.0%; Pred. No. 7.7e-165; Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps		expression of the tolerance to an drought) as compincilly as to the tolerance are a the tolerance are at the toler
1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQPH	09 00 00 00	produced by the an increased to variety of the or seed, an iso
61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQI 	120 CC CC CC CC CC CC CC CC CC CC CC CC CC	-a O H
121 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDTLDHIRAL 	180 CC XX SQ SQ	present sequenc Sequence 306 AA
		Query Match Best Local Similar: Matches 306; Con
VMEGYNWCQDKNVVTVPSAPNYCYRCGNWAAIMEIDETWNRSFLOFEPAPRQSEPDVTRK	300 OY	1 MPSYAD'          MPSYAD'
VMEGINNCQUANVVIVESARNICIRCGNMAAIMEIDEIMNKSFUQFEFAFKQSEFUVIKA. TPDYFL 306 	vo ove	61 DLIELE        61 DLIELE
301 TPDYFL 306	, ço	
RESULT 2 ABG74203 ID ABG74203 standard; protein; 306 AA.	ag &	121 TQVYGF 181 DRIQEV
ABG74203;	, a	
08-APR-2003 (first entry)	ò	241 VMEGYN
P. patens protein phosphatase PP2A-4.	qa	 241 VMEGYN
Plant; enzyme; PP2A-4; protein phosphatase; PHSRP; cold; transgenic; phosphatase stress related protein; environmental stress; drought; salt tolerance.	VS 40	301 TPDYFL        301 TPDYFL
Physcomitrella patens.		·
US2002152502-A1.	ABP9	RESULT 3 ABP98034 ID ABP98034 standa
17-OCT-2002.	XX	•••
06-APR-2001; 2001US-00828302.	XX	11-AUG-2003 (£
	XX X XX XX	Protein phospha Protein phospha BnPP2A-1; BnPP2
	E E X X	drought; salini
Da Costa E SilvaO, Bonnert HJ, Van Thielen N, Chen R, Ishitani M; WPT: 2001-198392/19	SO XX	Glycine max. WO2003020914-A2
MF1, 2003 130357.15. N-PSDB; ABX16239.	XX CO	13-MAR-2003.

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                                                                                                                                                                         Ď
                                                                                                                       on relates to a transgenic plant cell transformer Stress-Related Protein (PHSRP) coding nucleic a of the mucleic acid in the plant cell results in con an environmental stress (e.g. salt tolerance, compared to a wild type variety of the plant cell a transgenic plant comprising the novel plant cell the transgenic plant comprising the seed is true d tolerance to environmental stress as compared it the plant cell, an agricultural product produced isolated PHSRP coding nucleic acid, a vector comprising the nucleic acid, and producin ining PHSRP nucleic acid. The transgenic plant cell in a producin produced the plant cell in a producin a vector comprising the nucleic acid, and producin thing PHSRP nucleic acid. The transgenic plant cell is a Phosphatase Stress-Related Protein (PHSRP) in successive modifying stress tolerance of a luence represents the PHSRP, protein phosphatase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atase stress-related polypeptide; PPSRP; PpPP: 22A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3; 2A-3; plant tolerance; environmental stress; ; ity; cold; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRIGGKAPDTNYLEMGDYVDRGYYSVETVSLLVALKVRYRDRITI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant cell transformed by a Phosphatase Strer coding nucleic acid, useful for modifying s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1670; DB 6; Length 30. rity 100.0%; Pred. No. 7.7e-165; nservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEI FCLHGGLSPS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atase stress-related polypeptide GmPP2A-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ard; protein; 306 AA.
                                                                                     3C; 79pp; English.
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The present sequence represents a protein phosphatase stress-related polypeptide (PPSRP). The specification describes PPSRP polypeptides designated PPPP2A-1, PPPP-1, BNPP2A-2, BNPP2A-3, GMPP2A-1, GMPP2A-2, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-1, DPPP-1, BNPP2A-2, GMPP2A-3, GMPP2A-1, DPPP-1, BNPP2A-2, GMPP2A-3, GMPP2A-1, GMPP2A-3, GMPP2A-1, GMPP2A-3, GMPP2A-1, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-1, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP2A-3, GMPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDTLDHIRAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHTNGLSLISRAHQL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAPRQSEPDVTRK 300
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                                                                                                                                                                                                                                                                                                    New protein phosphatase stress-related polypeptide coding nucleic acid, useful for modulating plant's tolerance to an environmental stress such as drought, increased salinity and cold.
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                                                                                                                                                                         Da Costa E SilvaO;
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                                                                                                                                                                         Van Thielen N,
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91.5%; Pred. No. 3.1e-152;
ive 16; Mismatches 10;
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                                                                                                                                                                      Chen R, Ishitani M,
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TPDYFL 306
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OI 120 OI 120 AL 180 || AL 180 OL 240 || || 240 RK 300 || RK 300 9 9 PP-1; 1; cid, such 표<u>..</u>.첫 ä ö The present sequence represents a protein phosphatase stree polypeptide (PPSRP). The specification describes PPSRP poly designated PpPP2A-1, BnPP2A-1, BnPP2A-3, GmPP2A-2, GmPP2A-2, GmPP2A-2, GmPP2A-1, OSPP2A-1, OSPP2A-3, derived Physcomircalla patens, Brassica napus, Glycine max or Oryza polypeptides and polymucleotides are useful for modulating tolerance to an environmental stress such as drought or inc salinity and cold. They useful in identification a localization of Physcomircalla patens, Brassica napus, Glyc Oryza sativa and related organisms, mapping of genomes of c Protein phosphatase stress-related polypeptide; PPSRP; PpPF BPPPA-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3; GSPP2A-3; GSPP2A-3; plant tolerance; environmental stress; drought; salinity; cold; enzyme. otide coding reprised 92.6%; Score 1547; DB 6; Length 306 91.5%; Pred. No. 5e-152; ive 15; Mismatches 11; Indels Costa TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTBLESQIFCLHGGLSPE DLIELFRIGGNAPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRDRITI TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPS DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHTNC related to the above species, in a evolutionary and polyper structural studies, in determination of PBSRP regions regul function, modulation of PPSRP activity, modulation of metal or more cell functions and transmembrane transport of one c 1 MPSHADLERQIEQLMECKPLSESEVKALCDQARAILVEEWNVQPVKCPVI DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITI DRIGEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNG VMEGYNWCODKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLOFEPAF 1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPV Protein phosphatase stress-related polypeptide OsPP2A-5. Da New protein phosphatase stress-related polypeptide useful for modulating plant's tolerance to an envir as drought, increased salinity and cold. Van Thielen N, Ishitani M, Claim 18; Page 88; 107pp; English 05-SEP-2002; 2002WO-US028445. 05-SEP-2001; 2001US-0317305P Query Match Best Local Similarity 91.57 Matches 280; Conservative Chen R, WPI; 2003-300886/29 301 TPDYFL 306 (BADI ) BASF PLANT N-PSDB; ACC43354 Sequence 306 AA; WO2003020914-A2 Oryza sativa 13-MAR-2003 Bohnert HJ, 61 121 121 181 181 241 셤 g 요 g ò ò ð ð Š 셤 ò

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   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 37969.
                                                                                                        AAG31595 standard; protein; 306 AA
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91.1%; Score 1522; DB 3; Length 306;
Best Local Similarity 89.5%; Pred. No. 2e-149;
Matches 274; Conservative 17; Mismatches 15; Indels

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Gaps

1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQFH 60

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240 240 cid, such 유무성 ö New protein phosphatase stress-related polypeptide coding nuseful for modulating plant's tolerance to an environmental as drought, increased salinity and cold. VMEGFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENMEQNFLQFDPAF Protein phosphatase stress-related polypeptide; PPSRP; PpPF BPPPAA-2; BNPPAA-3; GMPP2A-1; GMPP2A-2; GMPP2A-3; Dant tolerance; environmental stress; drought; salinity; cold; enzyme. DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNG DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHNNC **VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAF** Da Costa Protein phosphatase stress-related polypeptide BnPP2A-1. Ishitani M, Van Thielen N, ABP98027 standard; protein; 306 AA. 05-SEP-2002; 2002WO-US028445. 05-SEP-2001; 2001US-0317305P. (BADI ) BASF PLANT SCI GMBH (first entry) Bohnert HJ, Chen R, WPI; 2003-300886/29. TPDYFL 306 rPDYFL 306 N-PSDB; ACC43342 WO2003020914-A2 Brassica napus. 11-AUG-2003 13-MAR-2003 241 ABP98027; 241 181 181 301 301 ABP98027 ID ABPS RESULT 6 ò g õ ò 셤 셤

The present sequence represents a protein phosphatase strespolygeptide (PPSRP). The specification describes PPSRP polydesignated PPPRA-1, PPPP-1, BNPP2A-1, BNPP2A-3, GMPP2A-2, GMPP2A-2, GMPP2A-1, OSPP2A-1, OSPP2A-3, derived Physcomircella patens, Brassica napus, Glycine max or Oryza polypeptides and polymucleotides are useful for modulating tolerance to an environmental stress such as drought or inc salinity and cold. They are also useful in identification a localization of Physcomitrella patens, Brassica napus, Glyc Oryza sativa and related organisms, mapping of genomes of c related to the above species, in a evolutionary and polyper structural studies, in determination of PRSR regions requi function, modulation of PPSRP activity, modulation of metab or more cell functions and transmembrane transport of one c Claim 7; Page 75; 107pp; English.

PPSRP

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Sequence 306 AA;

components

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                                                    The invention describes a recombinant DNA construct compris. polymucleotide consisting of a sequence encoding an amino a vailable in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The profit of the invention are also useful in physical arrays of moler plant breeding markers. The recombinant DNA construct is us improving plant tolerance to cold, heat, drought, herbicides osmocic conditions, pathogens or pests, for manipulating graphart cells by modification of the cell cycle pathway, for increased resistence to plant disease, for producing galactincased resistence to plant disease, for producing galacting increased resistence to plant disease, for producing galacting increasing srowth regulators, for increasing the rate of recombination in plants, for improving yield by modification photosynthesis or carbohydrate, nitrogen or phosphorus use or by providing improved plant growth and development under stress condition or for modifying seed oil or protein yield content. This is the amino acid sequence of a plant full lesponyment where the polypeptide that can be used in the recombinant DNA construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabobybridisation assay; genetic mapping; gene expression contratermination sequence.
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88.9%; Pred. No. 5.4e-149;
ive 23; Mismatches 11; Indels
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                             Claim 1; SEQ ID NO 72606; 15pp; English.
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Matches 272; Conservative
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Protein identification; signal transduction pathway; metabo hybridisation assay; genetic mapping; gene expression contratermination sequence.
                                             61 YDLIELFRIGGEAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRIT
                                                                                                                                     180 LDRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTW
                                                                                                                                                               LDRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAQQFNHTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG32348 standard; protein; 306 AA.
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99US-0126785P
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24-MAY-1999;
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19-APR-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a protein phosphatase stress-related polypeptide (PPSRP). The specification describes PPSRP polypeptides designated PpPP2A-1, PpPP-1, BnPP2A-2, BnPP2A-3, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, GmPP2A-1, 
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    241 VMEGFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQIEPDTTRK 300
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                                                                                                                                                                                                                                                                                                                                                                                        Protein phosphatase stress-related polypeptide; PPSRP; PpPP2A-1; PpPP-1; BPP2A-1; BPP2A-2; BPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3; OsPP2A-1; OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress; plant; drought; salinity; cold; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protein phosphatase stress-related polypeptide coding nucleic acid, useful for modulating plant's tolerance to an environmental stress such as drought, increased salinity and cold.
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                                                                                                                                                                                                                                                                                                                                             Protein phosphatase stress-related polypeptide OsPP2A-2.
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                                                                                                                                                                                                          ABP98036 standard; protein; 307 AA.
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                                                       1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQFH 60
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                                          Gaps
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                       Query Match 90.3%; Score 1508; DB 3; Length 306; Best Local Similarity 88.9%; Pred. No. 5.8e-148; Matches 272; Conservative 17; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                             Zea mays protein fragment SEQ ID NO: 44102.
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29-OCT-1999;
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PR 02-MC-11999 9918 0145218P

PR 03-MC-11999 9918 0145218P

PR 11-MC-11999 9918 0145218P
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PR 21-OCT-1999; 990S-0 PR 22-OCT-1999; 990S-0 PR 22-OCT-1999; 990S-0 PR 25-OCT-1999; 990S-0 PR 25-OCT-1999; 990S-0 PR 25-OCT-1999; 990S-0 PR 25-OCT-1999; 990S-0 PR 26-OCT-1999; 990S-0 PR 26-OCT-1999; 990S-0 PR 26-OCT-1999; 990S-0 PR 28-OCT-1999; 990S-0 PR 241 VMEGYNWCQDKN PO

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New recombinant DNA constructs useful in the field of bioch genetics, and in particular for producing transgenic plants biological characteristics.
                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 6733; 14pp; English.
                                                                                                                18-DEC-2003; 2003US-00739930.
                                                                                                                                               28-APR-2003; 2003US-00424599.
28-APR-2003; 2003US-00425115.
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Matches 270; Conservative
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                                                                                                                                                                                                (KOVA/) KOVALIC D K.
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                     Viridiplantae
                                                                                  28-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLV 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQFHD
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990S-0160768P-
990S-0160817P-
990S-0160818P-
990S-0160981P-
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Matches 268; Conserv
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The invention relates a recombinant DNA construct comprising polynacleotide with any of 5544 and clockide sequences (CDI polynacleotide with any of 5544 and incoding a polygeptide with any of 5544 incoding a polygeptide with any of 5544 incoding a polygeptide with any of 5545 incode is sequences is derived from which organism. Also included is producing a plant having an improved property, comprising that plant with a recombinant DNA construct comprising a promote plant with a recombinant DNA construct comprising a promote plant with a recombinant DNA construct comprising a promote plant with a recombinant DNA construct comprising the plant. The property is selected from improving plant cold to plant disease, for galactomannan production, casistance to plant disease, for galactomannan production, resistance to plant disease, for improving plant tolerance to herbicides, for increasing the homologous recombination in plants, for lignin production, comparance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving the photosynthesis, for medifying seed protein yield and/or content, for yield improved to carbohydrate, nitrogen or phosphorus use are and for yield improvement by providing improved plant growt development under at least one stress condition. The polynuc also encode a plant transcription factor. The methods and conditions, in particular for producing transgenic plants with belongered to extreme osmotic and drought conditions, and in the field, increasing plant tolerance to cold or heat, improving tolerance to extreme osmotic and drought conditions, and in the field of biocopherics are and colerance to extreme osmotic and drought conditions, and in the field of marver of molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arrays of molecules, plant breeding markers, computer-based analysis systems. The present sequence is one of the 5544 p sequences of the invention. Note: The sequence data for this not form part of the printed specification, but was obtaine
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                                                                      DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHNNGLSLISRAHQL 238
                                                                                              VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAPRQSEPDVTRK 300
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                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                          TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDTLDHIRAL
                                                            DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTWGLSLVARAHQL
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

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Database :

PIR 80:\*
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## ALIGNMENTS

phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chair phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chair Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 30.5ep1993 #sequence_revision 30.5ep-1993 #text_change C; Datession: S31169 E; Arino, J.; Perez-Callejon, E.; Cunillera, N.; Camps, M.; Posae Plant Mol. Biol. 21, 475-485, 1993 A; Title: Protein phosphatases in higher plants: multiplicity of A; Reference number: S31161; MUID: 93184204; PMID: 8382968 A; Acerosaion: S31161; MUID: 93184204; PMID: 8382968 A; Acerosaion: S31163 A; Residues: 1-306 ARI> A; Residues: 1-306 ARI> A; Cross-references: UNIPROT: Q07098; UNIPARC: UPI0000000846; EMBL: C; Superfamily: serine/threonine protein phosphatase, phosphoeste C; Keywords: iron; metalloprotein; phosphoric monoseter hydrolase F; 20-279/Domain: phosphoseterase core homology APE> F; 48-116/Domain: phosphoseterase core homology APE> F; 48-116/Domain: phosphoseterase core homology APE> F; 45, 56, 82/Binding site: iron (Asp., His, His) #statue	(EC 3.1.3.16) 2A-alpha catalytic chai iana (mouse-ear cress) ce_revision 30-Sep-1993 #text_change , E.; Cunillera, N.; Camps, M.; Posaɛ 5, 1993 MUID:93184204; PMID:8382968  **OOTO98; UNIPARC:UDI000000E46; EMBL: **OOTO98; UNIPARC:UDI000000E46; EMBL: **OOTO98; UNIPARC:UDI000000E46; EMBL: **OOTO98; UNIPARC:UDI000000E46; EMBL: **OOTO98; UNIPARC:UDI00000E46; EMBL: **OOTO98; UNIPARC:UDI00000E46; EMBL: **OOTO98; UNIPARC:UDI00000E46; EMBL: **OOTO99; UNIPARC:UDI00000E46; EMBL: **OOTO99; TAIL: MID: Marchicled tean core homology <pp> **OOTO99; ASP; Asp; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp> **OOTO99; ASP; Marchicled tean core homology <pp **ooto99;="" <pp="" core="" homolo<="" homology="" marchicled="" tean="" th=""><th>EP14a) - Arabidc 004  rrer, A. phosphatases in P NID:g166822; PIDN e homology; phost ;/threonine-specif</th></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp></pp>	EP14a) - Arabidc 004  rrer, A. phosphatases in P NID:g166822; PIDN e homology; phost ;/threonine-specif
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F;85,115,262/Active site: Asp, His, Tyr #status F;86,211/Binding site: substrate phosphate (Arg)	B 2; Length	
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Qy 1 MPSYADVDRQIEQLSECKPL	~ ~	FH 60
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Qy 61 DLIELFRIGGKAPDTNYLFW	DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITI	QI 120
Db 61 DLIELFRIGGNAPDTNYLFM	DLIELFRIGGNAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRLTI	01 120
Qy 121 TQVYGFYDECLRKYGNANVWI	TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPE	AL 180
Db 121 TQVYGFYDECLRRYGNANVW	TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIESQVFCLHGGLSPE	SL 180
Qy 181 DRIQEVPHEGPMCDLLWSDPI	DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNG	QL 240
Db 181 DRIQEVPHEGPMCDLLWSDP	DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAAQFNHNNG	ÓL 240
Qy 241 VMEGYNWCQDKNVVTVFSAPI	VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAF	RK 300
Db 241 VMEGFNWCQDKNVTVFSAPP	SIGENMEONFLO	RK 300
Qy 301 TPDYFL 306		
Db 301 TPDYFL 306		

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P,85,210/Binding site: substrate phosphate (Arg) #status predict.  Query Match  Best Local Similarity 88.2%; Score 1501.5; DB 2; Length 3' Best Local Similarity 88.2%; Pred. No. 3.5e-126;  Matches 270; Conservative 21; Mismatches 14; Indels  QY   IMPSOADUDROISECKPLESELEVKNLCDQARTILVEEWNVQPVKCPVT	RESULT 4  B96722  P06722  P06722  P06722  P06722  P06722  P06722  P06722  P06722  P06722  P06722  P0
REBULT 2 Sali61 Chosphartase (EC 3.1.3.16) 2A-alpha catalytic chain (clone EP8a) - Arabide Chosphartase thaliana (mouse-ear cress) C.Date: 30-Sep1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C.Accession: Sali61 C.Date: 30-Sep1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C.Accession: Sali61 C.Date: 30-Sep1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C.Accession: Sali61 C.Date: 30-Sep1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C.Accession: Sali61 C.Accession: Sa	61 DLIELFRIGGKAPDTNYLPMGDYUNGGYNSVETVSLLVALKVRYRDRITILRGNHESRQ1  121 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEBEIFCLHGGLSPSLDTLDHIRAL  121 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEBGYFCHGGLSPSLDTLDHIRAL  122 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEBGYFCHGGLSPSLDTLDHIRAL  123 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEBGYFCHGGLSPSLDTLDHIRAL  124 VMEGYNWCQDRAVYTVFSAPNYCYRCGNNAAILEIGERKBGNFLQFDFPRAPRQFEDVTRK  125 TTPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  302 TPDYFL 306  303 TPDYFL 306  304 TPDYFL 306  305 TPDYFL 306  306 TPDYFL 306  307 TPDYFL 306  307 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  309 TPDYFL 306  309 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  302 TPDYFL 306  303 TPDYFL 306  304 TPDYFL 306  305 TPDYFL 306  307 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  309 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  302 TPDYFL 306  303 TPDYFL 306  304 TPDYFL 306  305 TPDYFL 306  307 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  309 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  302 TPDYFL 306  303 TPDYFL 306  304 TPDYFL 306  305 TPDYFL 306  307 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  309 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  301 TPDYFL 306  302 TPDYFL 306  303 TPDYFL 306  304 TPDYFL 306  305 TPDYFL 306  306 TPDYFL 306  307 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306  308 TPDYFL 306

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C,Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change C;Accession: T03599 R;Suh, M.; Cho, H.; Kim, Y.; Liu, J.; Lee, H. Plant Mol. Biol. 36, 315-322, 1998 A;Title: Multiple genes encoding serine/threonine protein phosph: A;Reference number: Z14967; MUID:98145437; PMID:948443 A;Reference number: Z14967; MUID:98145437; PMID:948443 A;Reference number: Z14967; MUID:98145437; PMID:948443 A;Reference number: Z14967; MUID:98145437; PMID:948443 A;Reference: Z14967; MUID:98145437; PMID:948443 A;Reference: UNID: Remail Composition and C;Generics: University Xanth C;Generics: University Xanth C;Generics: University Xanth C;Generics: University Xanth C;Generics: University Xanth C;Superfamily: serine/threonine protein phosphatase; phosphoeste C;Keyords: iron; phosphoprotein phosphatase homology <ppp>F;44-112/Pomain: phosphosterase core homology <ppp>F;44-112/Pomain: phosphosterase core homology <ppp>F;44-112/Pomain: phosphosterase core homology <pre>F;44-112/Pomain: e></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></ppp></ppp></ppp>	Ouery Match Best Local Similarity Be.3%; Pred. No. 3.8e-121; Best Local Similarity Be.3%; Pred. No. 3.8e-121; Matches 264; Conservative 17; Mismatches 21; Indels Oy Matches 1 MPSYADVDRQIEQLSECKPLSELEVKNICDQARTILVEEWNVQPVKCPVT	RESULT 7 A27430 phosphorotein phosphatase (EC 3.1.3.16) 2-alpha catalytic chair phosphoprotein phosphatase 2A-alpha catalytic chair N; Alternate names: phosphoprotein phosphatase 2A-alpha catalytic C; Species: Sus scrofa domestica (domestic pig) C; Dacession: A27430 C; Dacesion: A27430 B; Stone, S.R.; Hofsteenge, J.; Hemmings, B.A. Biochemistry 26, 7215-7220, 1987 A; Title: Molecular cloning of cDNAs encoding two isoforms of the A; Reference number: A27430, MUID:88107662; PMID:2827745 A; Residues: 1-309 <sto. 1-309="" 21-282="" <ppp="" <sto.="" a;="" c;="" coss-references:="" domain:="" f;="" gb:mz="" homology="" hydrolase="" matalloprotein;="" monoester="" phosphatase="" phosphatase;="" phosphoeste="" phosphoprotein="" phosphoric="" protein="" residues:="" sentel-threonine="" superfamily:="" uniparc:upi0000000c15;="" uniprot:p05323;=""> F; 51-119/Domain: phosphoseterase core homology <ppp> F; 51-119/Domain: phosphoseterase core homology <prd> F; 51-119/Domain: phosphoseterase core homology <prd> F; 51-119/Domain: phosphoseterase core homology <prd> F; 88,118,265/Active site: A8p; His, Tyr #status predicted F; 88,118,265/Active site: A8p; His, Tyr #status predicted F; 89,214/Binding site: ubstrate phosphate (Arg) #status predict F; 89,214/Binding site: ubstrate phosphate (Arg) #status predict</prd></prd></prd></ppp></sto.>
	PESULT 5 T0339 probable phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain - rice (Species: Organ sativa (rice) C; Species: Organ sativa (rice) C; Date: 24-Mar-1399 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004 C; Accession: T0339 R; Chang, M.C.; Chen, X.; Wang, B. submitted to the EMBL Data Library, February 1996 A; Reference number: 214920 A; Reference number: 21492 A; Reference number: 214920 A; Reference number: 21492	Oy 61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSUTVSLLVALKVRYRDRITILRGNHESRQ1 120 61 DLIELFRIGGSPDTNYLFMGDYVDRGYYSUTVTLLVALKVRYRRRITILRGNHESRQ1 120 62 DLIELFRIGGSPDTNYLFMGDYVDRGYYSUTVTLLVALKVRYRRRITILRGNHESRQ1 120 63 DLIELFRIGGSPDTNYLFMGDYVDRGYYGSYGTTLLVALKRRYRRRITILLGNHESRQ1 120 64 DLIELFRIGGSPDTNYLFMGDYVDRGYYGTLLALIEHEIFCLHGGLSPSLDTLDHIRAL 180 65 DLIELFRIGGSPDTNYLFRANWRKYFDLFDLTALIEHEIFCLHGGLSPSLDTLDHIRAL 180 66 DLIELFRIGGSPDTNYRYFTDLFDYLPLTALIEHGISPSLDTLDHIRAL 180 67 DLIELFRIGGSPDTRKGGNAWWKYFTDLFDYLPLTALIEHGISPSLDTLDHIRAL 180 68 DLIELFRIGGSPDTRKGGNAWWKYFTDLFDYLPTALIEHGISPSLDTLDHIRAL 180 69 DRIGGSPDTRK 300 60 DLIELFRIGGSPDTRK 300 61 DLIELFRIGGSPDTRK 300 61 DLIELFRIGGSPDTRK 300 62 DLIELFRIGGSPDTRK 300 63 DLIELFRIGGSPDTRK 300 64 DLIELFRIGGSPDTRK 300 65 DLIELFRIGGSPDTRK 300 66 DLIELFRIGGSPDTRK 300 67 DLIELFRIGGSPDTRK 300 68 DLIELFRIGGSPDTRK 300 68 DLIELFRIGGSPDTRK 300 69 DLIELFRIGGSPDTRK 300 60 DLIELFRIGGSPDTRK 300 60 DLIELFRIGGSPDTRK 300 60 DLIELFRIGGSPDTRK 300 60 DLIELFRIGGSPDTRK 300 60 DLIELFRIGGSPDTRK 300 60 DLIELFRIGGSPDTRK 300 61 DLIELFRIGGSPDTRK 300 61 DLIELFRIGGSPDTRK 300 62 DLIELFRIGGSPDTRK 300 63 DLIELFRIGGSPDTRK 300 64 DLIELFRIGGSPDTRK 300 65 DLIELFRIGGSPDTRK 300 66 DLIELFRIGGSPDTRK 300 67 DLIELFRIGGSPDTRK 300 67 DLIELFRIGGSPDTRK 300 68

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Query Match  Best Local Similarity  Best Local Similarity  Best Local Similarity  Best Local Similarity  Batches 252; Conservative 32; Mismatches 17; Indels  Cy  Cy  Cy  ChypolegolsEckplsElevantLyBenvyOpvkcPvtVcGDII  Sillillillillillillillillillillillillill	PARBAL  phosphatase (EC 3.1.3.16) 2A-alpha catalytic chail C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change (c;Accession: S00104; 318812; A60240 R;daccara e Silva, O.B.; Alemany, S.; Campbell, D.G.; Cohen, P.T. R;da Cruz e Silva, O.B.; Alemany, S.; Campbell, D.G.; Cohen, P.T. A;Title: Isolation and sequence analysis of a cDNA clone encoding A;Accession: S00104 A;Moclecule type: Data and sequence analysis of a cDNA clone encoding A;Accession: S100104 A;Moclecule type: Data and sequence analysis of a cDNA clone encoding A;Accession: S18812 A;Accession: A60240 A;Accession: A60
Best Local Similarity   83.7%;   Pred. No. 1.6e-119;   Indels   0;   Gaps   0;   Matches   252;   Conservative   32;   Mismatches   17;   Indels   0;   Gaps   0;   Gaps   Conservative   32;   Mismatches   17;   Indels   0;   Gaps   0;   Gaps   Conservative   32;   Mismatches   17;   Indels   0;   Gaps   0;   Gaps   Conservative   Conservative   Conservative   Caps   Ca	

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RESULT 10 PART2A phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Accession: 306592; JS0060; PS0311; A36491 R;Posas, F.; Arino, J.	RESULT 11 S10371 phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chai ne C; Species: Bos primigenius taurus (cattle) C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change C; Accession: S10371; S32226 R: de Paoli-Roach, A.A.
Nucleic Acids Res. 17, 8369, 1989 A;Title: Nucleotide sequence of a rat heart cDNA encoding the isotype alpha of the catal A;Reference number: S06592; MUID:90045961; PMID:2554255 A;Accession: S06592 A;Molecule type: mRNA	submitted to the EMBL Data Library, March 1990 A;Description: Nucleotide sequence of a cDNA encoding the protei atase 2A alpha cata A;Reference number: S10371 A;Accession: S10371 A;Accession: S10371 A;Accession: S10371
3L:X160 .; Sugi	A, Residues: 1-309 < DEP> A, Residues: UNIPROT: P05323; UNIPARC: UPI000000C15; EMBL: NID: 9628; PIDN: CA A, Experimental source: aortic smooth muscle A, Fxperimental source: A. B. Chen, S.; Boynton, A. A.
A,Title: Molecular cloning of cDNA for the catalytic subunit of rat liver type 2A protein A,Reference number: J80060; MUID:89051001; PMID:2461222 A,Accession: J80060 A,Molecule type: mRNA A,Residues: 1-309 <a href="https://documents.com/refaces/light-refaces/light-refaces/">https://documents.com/refaces/</a> A,Residues: 1-309 <a href="https://documents///documents/">https://documents///d</a>	submitted to the EMBL Data Library, March 1993 A,Description: Nucleotide sequence of a bovine brain cDNA encodi lpha isotype of r A,Reference number: S32226 A,Accession: S32226 A,Status: preliminary A,Molecule type: mRNA
A;Accession: PS0311 A;Molecule type: protein A;Residues: 284,'P'.286-289,'L'.291-293 <ki2></ki2>	A,Residues: 1-309 <che> A,Cross-references: UNIPARC:UPI0000000C15; EMBL:X72858; NID:928E N:CAA51381.1; PII A:Experimental source: brain</che>
A;Cross-references: UNIPARC:UPI000017280B R;Wadzinski, B.E.; Heasley, L.E.; Johnson, G.L. J. Biol. Chem. 265, 21504-21508, 1990 A;Title: Multiplicity of protein serine-threonine phospharases in PC12 phonchromocytoma	C; Superfamily: serine/intendine protein phosphatase; phosphoeste e homology; phosp C; Keywords: iron; metalloprotein; phosphoric monoester hydrolase /threonine-specif F; 23-282/Domain: phosphorotein phosphatase homology <ppp> F: 51-119/homain: phosphoesterse ore homology <ppp> F: 51-119/homain: phosphoesterse ore homology <ppp></ppp></ppp></ppp>
	F;57,59,85/Binding site: iron (Asp., His, Mas) #status predicted F;85,117,167,241/Binding site: zinc (Asp., Asn., His, His) #status F;88,118,265/Active site: Asp., His, Tyr #status predicted F;88,118,265/Active site: substrate phosphate (Arg) #status predict
A; Cross-references: UNIPARC: UPI000000049B; GB:MS843B; NID:g206300; PIDN:AAA41911.1; PID: C; Superfamily: serins/threonine protein phosphatase; phosphoesterase core homology; phosp C; Kaywords: iron; metalloprotein; phosphoric monoster hydrolase; serine/threonine-specifF: 23-282. Domain: phosphorotein phosphatase homology, ppp.	Query Match Best Local Similarity 83.7%; Pred. No. 1.6e-119; Matches 252; Conservative 32; Mismatches 17; Indels s 0;
F;51-119/Domain: phosphoesterase core homology CEC> F;57,59,85/Binding site: iron (Asp, His, Asp) #status predicted F;87,117,167,241/Binding site: site: (Asp, Asn, His, His) #status predicted F;85,117,167,241/Binding site: site: and the fire or and the f	Qy 6 DVDRQIEQLSECKPLSELEVRALCDQARTILVEEWNVQPVKCPVTVCGD1 EL 65   :: :
F;89,214/Binding site: substrate phosphate (Arg) #status predicted  Query Match  Rest Local Similarity 93.7% Drad No. 110.110.	Qy 66 FRIGGKAPDINYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNF YG 125
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DD 9 ELDQWIEQLNECKQLSESQVKSLCEKAKETLTKESNVQEVRCPVTVCGDVHGQFHDLMEL 68	Qy 186 VPHEGPMCDLLWSDPDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVA GY 245

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A; Accession: \$12961 A; Status: not compared with conceptual translation A; Molecule type: mRNA A; Residues: 1-309 <org> A; Residues: 1-309 <org> C; Ganetice: UNIPROF: P23696; UNIPARC: UPI0000007461; GB: X5:</org></org>	A;Gene: FlyBase:Pp2A-28D A;Cross-references: FlyBase:FBgn0004177 A;Map position: 2L 28D2-4 C;Superfamily: serine/threonine protein phosphatase; phosphoeste: C;Keywords: iron; metalloprotein; phosphoric monoester hydrolase F:23-282/Domain: phosphortein phosphatase homoloay <ppp></ppp>	F;51-119/Domain: phosphoeserase core homology <pes, #status="" (arg)="" (asp,="" active="" asn,="" asp)="" asp,="" binding="" f;57,59,85="" f;87,59,85="" f;88,117,167,241="" f;88,118,265="" f;89,214="" his)="" his,="" iron="" linding="" phosphate="" predict.<="" predicted="" site:="" substrate="" td="" tyr="" zinc=""><td>Query Match Best Local S Matches 249 Oy 6</td><td>DD 9 DEDQWIEGENEEUNGEIEIQVRIEGENAGEVREFVINGEVREFVINGEUNGEVREFVINGEUNGEVREFVINGEUNGEVREFVINGEUNGEVREFVINGEUNGEVREFVINGEUNGEVREFVENEUNGEVRUNGEVRUNGENAGENUNGENAGENUNGENUNGENAGENUNGENAGENUNGENUN</td><td>Qy 126 FYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDTLD)                                      </td><td>Qy 186 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVAN                                      </td><td>Qy 246 NWQQDKNVYTVFSAPNYCYRCGNWAAIMEIDETWNRSFLQFEPAPRQSEP                                     </td><td>Qy 306 L 306   309 L 309</td><td>RESULT 14 PAHUSD PAHOSD phosphoprotein phosphatase (EC 3.1.3.16) 2-beta catalytic chain N,Alternate names: protein phosphatase 2A-beta isoform catalytic</td><td>C;Species: Homo saplens (man) C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change   C;Accession: B37135; S01985; B32143; S09378; A34060 R;Khaw-Goodall, Y:, Mayer, R.E.; Maurer, F.; Stone, S.R.; Hemmin: Richemistry 30, 89-97, 1991.</td><td>A;Title: Structure and transcriptional regulation of protein pho: A;Reference number: A37135; MUID:91105105; PMID:1846293 A;Accession: B37135 A;Molecule type: DNA</td><td>A; KeBidueB: 1-309 KKHE&gt; A; Cross-referenceB: UNIPROT:P11082; UNIPARC:UP10000000CC2; GB:M6: R; Hemmings, B.A.; Wernet, W.; Mayer, R.; Maurer, F.; Hofsteenge, Nncleic Acids Res. 16. 11366, 1988</td><td>A;Title: The nucleotide sequence of the cDNA encoding the human. A;Reference number: S01985; MUID:89083568; PMID:2849765 A;Accession: S01985 A;Molecule type: mRNA</td><td>A; KeBidueB: 1-309 chEM&gt; A; Cross-references: UNIPARC:UP10000000CC2; EMBL:X12656; NID:g355: A; Arino, J.; Woon, C.W.; Brautigan, D.L.; Miller Jr., T.B.; John: Proc. Natl. Acad. Sci. U.S.A. 85, 4252-4256, 1988 A; Title: Human liver phosphatase 2A: cDNA and amino acid sequence</td><td></td></pes,>	Query Match Best Local S Matches 249 Oy 6	DD 9 DEDQWIEGENEEUNGEIEIQVRIEGENAGEVREFVINGEVREFVINGEUNGEVREFVINGEUNGEVREFVINGEUNGEVREFVINGEUNGEVREFVINGEUNGEVREFVINGEUNGEVREFVENEUNGEVRUNGEVRUNGENAGENUNGENAGENUNGENUNGENAGENUNGENAGENUNGENUN	Qy 126 FYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDTLD)	Qy 186 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVAN	Qy 246 NWQQDKNVYTVFSAPNYCYRCGNWAAIMEIDETWNRSFLQFEPAPRQSEP	Qy 306 L 306   309 L 309	RESULT 14 PAHUSD PAHOSD phosphoprotein phosphatase (EC 3.1.3.16) 2-beta catalytic chain N,Alternate names: protein phosphatase 2A-beta isoform catalytic	C;Species: Homo saplens (man) C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change   C;Accession: B37135; S01985; B32143; S09378; A34060 R;Khaw-Goodall, Y:, Mayer, R.E.; Maurer, F.; Stone, S.R.; Hemmin: Richemistry 30, 89-97, 1991.	A;Title: Structure and transcriptional regulation of protein pho: A;Reference number: A37135; MUID:91105105; PMID:1846293 A;Accession: B37135 A;Molecule type: DNA	A; KeBidueB: 1-309 KKHE> A; Cross-referenceB: UNIPROT:P11082; UNIPARC:UP10000000CC2; GB:M6: R; Hemmings, B.A.; Wernet, W.; Mayer, R.; Maurer, F.; Hofsteenge, Nncleic Acids Res. 16. 11366, 1988	A;Title: The nucleotide sequence of the cDNA encoding the human. A;Reference number: S01985; MUID:89083568; PMID:2849765 A;Accession: S01985 A;Molecule type: mRNA	A; KeBidueB: 1-309 chEM> A; Cross-references: UNIPARC:UP10000000CC2; EMBL:X12656; NID:g355: A; Arino, J.; Woon, C.W.; Brautigan, D.L.; Miller Jr., T.B.; John: Proc. Natl. Acad. Sci. U.S.A. 85, 4252-4256, 1988 A; Title: Human liver phosphatase 2A: cDNA and amino acid sequence	
Db 189 VPHEGPMCDLLMSDPDDRGGWGISPRGAGYTFGQDISETFNHANGLTLVSRAHQLVMEGY 248  Qy 246 NWCQDKNVVTVESAPNYCYRCGNMAAIMEIDETWNRSFLQFEBAPRGSEPDVTRKTDDYF 305	Qy 306 L 306 Db 309 L 309 RESULT 12	\$20348 phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain - clawed frog c;Species: Xenopus sp. (clawed frog) C;Species: Xenopus sp. (clawed frog) C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004 C;Accession: S20348 R;Cormier, P.; Osborne, H.B.; Bassez, T.; Poulhe, R.; Belle, R.; Mulner-Lorillon, O.	FEBS Lett. 295, 185-188, 1991 A;Title: Protein phosphatase 2(A) from Xenopus oocytes. Characterization during meiotic A;Reference number: \$20348; MUID:92111736; PMID:1662645 A;Accession: \$20348 A;Molecule type: mRNA A;Rolecules: 1-309 <cor></cor>	A; Cross-reterences: UNIPAKC: UPIUUUUUFES11; EMBL:X62114 C; Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos C; Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-speci F; 23-282/Domain: phosphoprotein phosphatase homology < PPP> F; 51-119/Domain: phosphoprotein phosphatase core homology < PPP> F; 51-119/Domain: phosphoprotein phosphatase core homology < PPP> F; 51-119/Domain: phosphoprotein phosphatase core homology < PPEC> F; 51-119/Domain: phosphoprotein phosphatase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC> F; 51-119/Domain: phosphosterase core homology < PPEC>	F,57,57,57,57,57,107,107,107,107,107,107,107,107,107,10	Query Match 85.1%; Score 1421; DB 1; Length 309; Best Local Similarity 83.4%; Pred. No. 5.4e-119; Matches 251; Conservative 32; Mismatches 18; Indels 0; Gaps 0;	OY 6 DVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQFHDLIEL 65 ::	Oy 66 FRIGGKAPDTNYLFWGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQITQVYG 125	QY 126 FYDECLEKYGNANVWKYPTDLFDYLPLTALIEHBIFCLHGGLSPSLDTLDHIRALDRIDE 185	Db 189 VPHEGPMCDLLMSDPDDRGGWGISPRGAGYTFGQDISETFNHANGLTLVSRAHOLVMEGY 248  Qy 246 NWCQDRNVVTRSAPNYSCGNMAAIMEIDETWNRSFLQFERPRQSEDDYRKTFDYF 305		DD 309 L 309 RESILT 13	\$12961 phosphoprotein phosphatase (EC 3.1.3.16) 2A-28D catalytic chain - fruit fly (Drosophila C;Species: Drosophila melanogaster C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004	C;Accession: S12951 R;Orgad, S.; Brewis, N.D.; Alphey, L.; Axton, J.M.; Dudai, Y.; Cohen, P.T.W. R:Orgad, S.; 44-48, 1990 A;Title: The structure of protein phosphatase 2A is as highly conserved as that of protein \$\frac{2}{2}\$, Reference number: \$12961; MUID:91085575; PMID:2175718	4

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A; Map position: 8p12-8p11.2 C; Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos C; Keywords: iron; metalloprotein; phosphoric monoster hydrolase; serine/threonine-speci F: 73-287 Unemain: phosphoryctein phosphatase	П ,
F;51-119/Domain: phosphoesterase force homology <pre>/Fig. 119/Domain: predicted force force homology <pre>/Fig. 119/Domain: predicted force for</pre></pre></pre></pre></pre></pre>	
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RESULT 15 PARRZB phosphoprotein phosphatase (EC 3.1.3.16) 2A-beta catalytic chain - rabbit phosphoprotein phosphatase (EC 3.1.3.16) 2A-beta catalytic chain - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004 C;Accession: S00220 R;da Cruz e Silva, O.B.; Cohen, P.T.W. FEBS Lett. 226, 176-178, 1987	

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CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

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PRIOR PELLING DATE: 2000-03-03

PRIOR FILING DATE: 2000-03-04

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARRE: CURPARELCATION NUMBER: 60/178,965

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARRE: CURPALSEGFORMATHER Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                             186 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVA
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                                                                                                                                                                                                                                                                 85.4%; Score 1427; DB 2; Length 355
83.7%; Pred. No. 4.1e-151;
tive 32; Mismatches 17; Indels
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASICSEQ for Windows Version 4.0
SEQ ID NO 11414
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.7
Matches 252; Conservative
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
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ORGANISM: Homo sapiens
                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11414
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS: METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELLING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Glot, Loic:
| APPLICANT: Mansfield, Traci A. |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| FILE OF INVENTION: 1596-542 |
| PRIOR APPLICATION NUMBER: 60/127,352 |
| PRIOR FILING DATE: 1999-04-01 |
| PRIOR FILING DATE: 2000-02-01 |
| PRIOR FILING DATE: 2000-02-01 |
| NUMBER OF SEQ ID NOS: 1387 |
| SOFTWARE: CuraPatSeqFormatter Version 0.9 |
| LENGTH: 309 |
| LENGTH: 309 |
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LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P05323
US-09-538-092-884
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ORGANISM: Homo sapiens
  301 TPDYFL 306
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84.5%; Score 1411; DB 2; Length 309
Best Local Similarity 82.4%; Pred. No. 2e-149;
Matches 248; Conservative 34; Mismatches 19; Indels
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i OTHER INFORMATION: Polypeptide Accession Number P11082
US-09-538-092-902
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PB 309 L 309  RESULT 6 US-09-949-016-11335 Sequence 11335, Application US/09949016 Fatent No. 6812339 GRNERAL INFORMATION: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION FILE REFERENCE: CLOOL307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 FRIOR FILING DATE: 2000-10-03		246 246 251 306 311 311 3ULT 7 509-9768 Sequence 10, Patent No. 6 GENERAL IN APPLIL TITLE TITLE NUMBE
DD   SELDOWVEQLNECKQLNENOVRTLCERAKEILTKESNVQEVRCPVTVCGDVHGQFHDLMEL 68	SOCIATED DETECTION AND U	Query Match         84.5%;         Score 1411;         DB 2;         Length 309;           Best Local Similarity         82.4%;         Pred. No. 2e-149;           Matches 248;         Conservative 34;         Mismatches 19;         Indels 0;         Gaps 0;           6b         DUDROIDEOLSECKPLSELEVRALCDOARTILVEEWNVOPVKCOVTVCGDIHGOFHDLIEL 68         65         66         ELDQWYZQLARCKQLARCKQLARCKTCEKAREILTRESNVOEWRCPTVCGDYHGOFHDLMEL 68         68           6c         FRIGGRAPDTNYLFMGDYVDRGYYSVETVELLYALKVRYRDRITILRGAHESROITQVYG 128         69         FRIGGRAPDTNYLFMGDYVDRGYYSVETVELVALKVRYPERITILRGAHESROITQVYG 128         69           7c         126         FYDECLRKYGNANVWKYFTDLFDYLPLTALIBHEIFCLHGGLSPSLDTLDHIRALDRIOE 185         189           8c         FRIGGRSPDTNYLFMGDYVDRGYYSVETVELYALKVRYPERITILRGAHESROITQVYG 128         189           8c         FRIGGRSPDTNYLFMGDYVDRGYYSVETVELYALKVRYPERITILRGAHESROITQVYG 128         189           8c         FRIGGRSPDTNYLFMGDYVDRGYYSVETVELYALVALKVRYPERITILLGALBEDTLARALDLANGE 188         189           8c         FYDECLRKYGNANVWKYFTDLFDYLPLTALIBHEIFCLHGGLSPSIDTLDHIRALDRIOE 188         189           8c         FYDECLRKYGNANVWKYFTDLFDYLPLTALIBHEIFCLHGGLSPSIDTLDHIRALDRIOE 188         189           8c         186         VPHEGPROLLMSDPDDRGGWGISPRGGYTFGQDISETRINAGLTLUSRALDLANGEY 248           8c         186         VPHEGPROLLMSDPDDRGGWGI

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/S 317
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CURRENT APPLICATION NUMBER: US/09/487,558B
RIOR APPLICATION WUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
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                                                                                                                                                                                                                                          77.3%; Score 1291; DB 2; Length 377 76.3%; Pred. No. 7.9e-136; ive 34; Mismatches 37; Indels
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              PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SEQ ID NO 270
LENGTH: 377
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GENERAL INFORMATION:
                                                                                                                                                        TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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2000-01-19
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Royer, John
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Holtzman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
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CURRENT FILING DATE:
                                                                                                                                                                                                   US-09-487-558B-270
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LENGTH: 369
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILS REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 325;
                ZIP: 01930

COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: Dell PC
OPERATING SYSTEM: MS DOS
OPERATING SYSTEM: MS DOS
OFTWARE: Microsoft Word version 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/190,976B
FILING DATE: 12-No. 6815187-1998
CLASSIFICATION: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.4%; Score 1326; DB 2; Length 3 Best Local Similarity 81.6%; Pred. No. 7.5e-140; Matches 235; Conservative 32; Mismatches 21; Indels
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-190-976B-10
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Patent No. 694936
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Gali, Brian
APPLICANT: Hedit, Perer
APPLICANT: Madden, Kevin
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. 6949356man, Thea
APPLICANT: Royer, John
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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US-09-487-558B-270
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YG 131
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QE 191
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GY 251
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YF 311
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|EL 71
                               Craig et al.
DLYMORPHISMS IN KNOWN GENES ASSOCIATED
MITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                               58.3%; Score 973; DB 2; Length 312; 58.8%; Pred. No. 2.6e-100; tive 41; Mismatches 83; Indels
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YIFWGDFVDRGYYSLETFTYLLALKAKWPDRITLLRGNE
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OR DIAGNOSTICS AND THERAPEUTICS
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UWBER: US/09/248,796A

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98-02-13

198-08-13

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UMBER: US/09/949,016

2000-04-14,755

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MER: 60/237,768

000-10-03

MER: 60/231,498

000-09-08

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ion US/09949016
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3L 241

3Y 304

2Y 301

CANDIDA ALBICANS

Db 182 IPHEGPFCDLMMSDPEDIETWAVSPRGAGWLFGSRVTSEFNHINNLDLVCI Qy 246 NWC-QDKNVTIVFSAPNYCYRCGNWAAIMEIDETWINRSPLQFEPAPRQSEI	4;			0,		Query Match 47.1%; Score 786; DB 2; Length 271; Best Local Similarity 66.2%; Pred. No. 2e-79; Matches 141; Conservative 32; Mismatches 40; Indels	ing the catalytic subunit A that regulates flowering Db	US/09/916,338A   G3 IELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRPRHTILR(	Qy 123 VYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLD'	Oy 183 IQEVPHEGPMCDLLWSDPDDRCGWGISFRGAGY 215	11, Mismatches 3 VVRNLCDARTILVEEMNV :     :     :           ILQLLCEYVKEILIEESNV DRGYYSVETVSLLVALKV DRGYNSLDVFTILLILIKAL DRFGYNSLDVFTILLILIKAL
TYPE: PRT ORGANISM: Candida albicans -09-248-796A-18310	Query Match Best Local Similarity 56.3%; Pred. No. 3.2e-99 Matches 175; Conservative 55; Mismatches 6 B DRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQP	1	124 TGFTDEDILANGUANNAN TETDEFDIEDIEDIEDIEDIEDIEDIEDIEDIEDIEDIEDIEDIED	244 GYNW-CQDKNVVTVFSAPNYCYRCGNWAAIMEIDETFM [::::::: :	RESULT 13 US-09-916-338A-2 ; Sequence 2, Application US/09916338A	; FACERIL NO. 928023. ; APPLICANT: KANG, JEONG-GU ; APPLICANT: SONG, PILL_SOON	PARK, CHUNG-MO WYENTION: Nuclear acid molecule encodis WYENTION: of a Protein Phosphatase 2A WYENTION: time in plants	FILE REFERENCE: P66903USO CURRENT APPLICATION NUMBER: US/09/916,338A CURRENT FILING DATE: 2002-02-15 NUMBER OF SEQ ID NOS: 4	OCFIWARE: Patentin Ver. 2.1 OC ID NO 2 LENGTH: 303 TYPE: PRT	ORGANISM: Pisum sativum -09-916-338A-2 Query Match	170; Conservative 51; Mismatches 8  6 Didonischer Secretselevralive 8  2 Didoniskvendoghliedelije

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OR 182 : | UR 238

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                                                                                                                                                                                                                                      6 DVDRQIEQLSE----CKP----LSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDLHG 57
                                                                                                                                                                                                                                                        12; Gaps
                                                                                                                                                                             Query Match 45.3%; Score 757; DB 2; Length 323; Best Local Similarity 46.3%; Pred. No. 4.6e-76; Matches 142; Conservative 66; Mismatches 87; Indels
) NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 1093

LENGTH: 3.23

TYPE: PRT

ORGANISM: Homo sapiens
FRATURE:

NAME/KEY: misc_feature

LCCATION: (0)...(0)

COATION: (0)...(0)

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Search completed: December 9, 2005, 10:25:06 Job time : 47 secs

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Result Š.

Appl 936, Appl 051, 053, 55, A 43, A 6093, 935, 1175, 1175, 1175, 1175, Appl 1

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Sequence 13. Application US/09828302
; Sequence 13. Application US/09828302
; Patent No. US20020152502A1
; GENERAL INPORMATION:
   APPLICANT: COSTA E SILVA, OSWALDO DA APPLICANT: CARAN, ROUTING
   APPLICANT: CHEN, ROUTING
   APPLICANT: CHEN, ROUTING
   TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND PRITE OF INVENTION: IN PLANTS
   TITLE OF INVENTION: IN PLANTS
   CURRENT APPLICATION NUMBER: US/09/828,302
   CURRENT FILING DATE: 2001-08-20
   PRIOR APPLICATION NUMBER: 60/196,001
   PRIOR FILING DATE: 2000-04-07
   NUMBER OF SEQ ID NOS: 46
   NUMBER PERCENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1670; DB 3; Length 3C 100.0%; Pred. No. 7.9e-166; cive 0; Mismatches 0; Indels
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       US-10-425-115-287936
US-10-236-699-30
US-10-425-114-56755
US-10-425-114-40943
US-10-425-114-40943
US-10-424-599-166855
US-10-437-963-174105
US-10-437-967-103935
US-10-437-967-103935
US-10-434-599-191175
US-10-739-930-10910
US-10-739-930-10910
US-10-369-493-2498
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US-10-369-493-1551
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US-10-369-493-1568
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US-09-828-302-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 306; Conservative
TPDYFL 306
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LENGTH: 306
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                                                                      December 9, 2005, 10:18:01; Search time 119 Seconds
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                        1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
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                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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; NUMBER OF SEQ ID NOS: 43; SOFWARRE: Patentin Ver. 2.1; SEQ ID NO 22; LENGTH: 306; TYPE: PRT; TYPE: PRT; CREANISM: Glycine max US-10-236-699-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OKGANISM: Oryza sativa
US-10-236-699-32
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Best Local Similarity
Matches 280; Conserv
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                                                                                    Sequence 13, Application US/10764259

Publication No. US20040148658A1

Publication No. US20040148658A1

Publication No. US20040148658A1

PUBLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: CHENA, NOCHA

APPLICANT: CHENA, ROUTING

APPLICANT: CHENA, ROUTING

APPLICANT: SINTENCE: 16313-0029

TITLE OF INVENTION: IN PLANTS

FILE REFERENCE: 16313-0029

CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: 60/196,001

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

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APPLICANT: CHEN, RUCYING
APPLICANT: CHEN, RUCYING
APPLICANT: SHITTANI, MANABU
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: COSTA E SILVA, OSWALDO DA
TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
TITLE OF INVENTION: METHODS OF USE IN PLANTS
FILE REPERENCE: 16313-0161
CURRENT APPLICATION NUMBER: US/10/236,699
CURRENT APPLICATION NUMBER: US/202-09-05
PRIOR APPLICATION NUMBER: 60/317,305
PRIOR FILING DATE: 2001-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 100.0%; Score 1670; DB 4; Length 306; Local Similarity 100.0%; Pred. No. 7.9e-166; les 306; Conservative 0; Mismatches 0; Indels 0
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Publication No. US20030150028A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Physcomitrella patens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 TPDYFL 306
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Best Local S:
Matches 306
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APPLICANT: CHEMIN, RUCHAGE
APPLICANT: SHITANI, MANABU
APPLICANT: TISHITANI, MANABU
APPLICANT: VAN TITELEN, WOCHAL
APPLICANT: COSTA E SILVA, OSWALDO DA
TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPE:
TITLE OF INVENTION: METHODS OF USE IN PLANTS
FILE REFERENCE: 16313-0161
CURRENT APPLICATION NUMBER: US/10/236,699
CURRENT PILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: 60/317,305
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 32
LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITI
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                                                                                                                                                                                                 61 DLIELFRIGGNAPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRDRITI.
                                                                                                                                                                                                                                                                 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPS.
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  Length 306
                                                                                                                                                                             DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITI
                                             Indels
Query Match 92.8%; Score 1549; DB 4; Best Local Similarity 91.5%; Pred. No. 3.7e-153; Matches 280; Conservative 16; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Sequence 32, Application US/10236699; Publication No. US20030150028A1 GENERAL INFORMATION: APPLICANT: BOHNERT, HANS J.
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ated With

	; APPLICANT: La Rosa, Thomas J. ; APPLICANT: Kovalic, David K. ; APPLICANT: Zhou, Yihua ; APPLICANT: Cao, Yongwei		; CURRENT FILING DATE: 2003-04-28 ; NUMBER OF SEQ ID NOS: 369326 ; SEQ ID NO 345205 ; LENGTH: 306	TYPE: PRT CORGANISM: Zea mays FEATURE:	ORMATION: Clone ID: MRT4577_77994C.1.pep -345205	Query Match 91.1%; Score 1521; DB 4; Length Best Local Similarity 88.9%; Pred. No. 3.1e-150; Matches 272; Conservative 23; Mismatches 11; Indele	Qy 1 MPSYADVDRQIBQLSECKPLSELBVRNLCDQARIIJVEBWNVQPVKCPVI	Qy 61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITI 	Qy 121 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSP4	OY 181 DRIQBVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNG	OY 241 VMEGYNWCODKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAF	Oy 301 TPDYFL 306			) HELLCANT: Znou, Yinda HELLCANT: Kovalic, David K. APPLICANT: Screen, Steven E HELLCANT: Tabaska, Jack E			; NUMBER OF SEQ ID NOS: 73128 ; SEQ ID NO 72606	PRINCIA: SIZ
OY 121 TQVYGFYDECLEKYGNANVWKYFTDLFDYLPLALIEHEIFCLHGGLSPSLDTLDHÍRAL 180 		QY 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAPRQSEPDVTRK 300 [	Oy 301 TPDYFL 306        Db 301 TPDYFL 306	RESULT 5	US-10-238-899-8 Sequence 8, Application US/10236699 ; Publication No. US20030150028A1	; GENERAL INFORMATION: ; APPLICANT: BOHNERT, HANS J. ; APPLICANT: CHEN, RUOYING	APPLICANT: VAN THIELEN, WORDED APPLICANT: VAN THIELEN, OSWALDO DA APPLICANT: COSTA E SILVA, OSWALDO DA TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND	FILE REFERENCE: 16313-0161 FILE REFERENCE: 16313-0161 CURRENT APPLICATION NUMBER: US/10/236,699 CURRENT FILING DATE: 2002-09-05	PRIOR APPLICATION NUMBER: 60/317,305 PRIOR FILING DATE: 2001-09-05 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver. 2.1	SEQ ID NO 8 LENGTH: 306 TYPE: PRT ORGANISM: Brassica napus	OS-IU-236-699-8  Query Match Best Local Similarity 88.9%; Pred. No. 3.1e-150; Matches 272: Conservative 70: Mismarches 14: Indale 0: Gane		QY 61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQ1 120	Qy 121 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDFLDHIRAL 180	181 DRIQEVPHECPMCDLLWSDPDDRCGWGISPRGAGYTFQQDIAEQFNHTNGLSLVARAHQL	Db 181 DRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIATQFNHTNGLSLISRAHQL 240  Qy 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETWNRSFLQFEPAPRQSEPDVTRK 300	Db 241 WHGGYNWCQEKNVVTVFSARNYCYRCGNWAAILEIDENMDONFLQFDPAPRQVEPETTRK 300	Qy 301 TPDYFL 306	301 IPDIED

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AL 180 :| SL 180

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; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE90H04_FLI.pep US-10-425-114-72606	QY         180         LDRIQEVPHECPMCDLIMSDPDDRCGWGISPRGAGYTFQQDIAEQFNHTN         1Q         23           Db         181         LDRIQEVPHECPMCDLIMSDPDDRCGWGISPRGAGYTFQQDIAEQOFNHTN         4Q         24	239
Query Match 90.9%; Score 1518; DB 4; Length 312; Best Local Similarity 88.9%; Pred. No. 6.7e-150; Matches 272; Conservative 23; Mismatches 11; Indels 0; Gaps 0;	240 LUMEGYNWCQDKNVVTVPSAPNYCYRCGNMAAIMBIDETMNRSFLQFBPA	299
QY 1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEBNNVQPVKCPVTVCGDIHGQFH 60	LETGENMUQNFLUCFUFA.	000
Qy 61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQI 120 Db 67 DLIELFRIGGDAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQI 126	Db 301 KTPDYFL 307 RESULT 9	
Qy     121 TQVYGFYDECLRKYGNANVMKYFTDLPDYFDZLFLIEHEIFCLHGGLSPSLDTLDHIRAL 180       Db     127 TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIENQIFCLHGGLSPSLDTLDNIRAL 186	US-10-437-963-143206; ; Sequence 143206, Application US/10437963 ; Publication No. US20040123343A1 ; GENERAL INFORMATION:	
Qy 181 DRIQEVPHEGEMCDLLWSDFDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQL 240	; APPLICANT: La Rosa, Thomas J.; APPLICANT: Kovallic, David K.; APPLICANT: Zhou, Yihua; APPLICANT: Cao, Yongwei	
Qy 241 VMEGYNWCQDKNVVTVPSAPNYCYRCGNWAAIMEIDETWNRSFLQFEPARQSEPDVTRK 300 Db 247 VMEGFNWCODKNVTVTVFSAPNYCYRCGNWAILEIGENMDONFLOFPPARROIEPDWTRK 306		
301 TPDYFL 306	les and Other Mold for Plant Improva	sociated
Db 307 TPDYFL 312	; CURRENT APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-05-14; WIMMER OF SECTION OF	
RESULT 8 US-10-236-699-26 ; Sequence 26, Application US/10236699 ; Publication No. US20030150028A1 ; GENERAL INFORMATION: ; APPLICANT: PORINERT. ; APPLICANT: CHEN, RUOYING	; NOT 143206 ; LENGTH: 307 ; TYPE: PRT ; ORGANISM: Oryza sativa ; PEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT4530_44137C.1.pep	
至	Query Match 90.3%; Score 1508.5; DB 4; Length 30 Best Local Similarity 88.6%; Pred. No. 6.4e-149; Matches 272; Conservative 23; Mismatches 11; Indels 3	1;
	KPLSELEVKOLCDQARTILVEEWNVQPVKCPV 2F	60
	QY         60 HDLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRIT.         3Q 13           bb         61 YDLIELFRIGGEAPDTNYLFMGDYVDRGYYSVETVSLLVALKVRYRDRIT.         3Q 13	119
; SEQ ID NO 26 ; LENGTH: 307 ; TYPE: PRT ; ORGANISM: Oryza sativa	QY         120 ITQVYGFYDECLRKYGNANVWKYFTDLFDYLFLTALIEHEIFCLHGGLSF:         3A 1'           Db         121 ITQVYGFYDECLRKYGNANVWKYFTDLFDYLFLTALIENQVFCLHGGLSF:         3A 1'	179 180
US-10-216-699-26 Query Match 90.3%; Score 1508.5; DB 4; Length 307; Best Local Similarity 88.6%; Pre61.No. 6.4e-149; Matched 777: Concornation of Matched 10.10.10.10.10.10.10.10.10.10.10.10.10.1	ō— <b>ō</b>	239
1 MP-SYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQF 59  1 MP-SYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQF 59  1 MPSSHGDLDRQIAQLRECKHARGESVRALCEQAKAILAMEWNVQPVRCPVTVCGDIHGOF 60	Qy 240 LVMEGYNWCQDKAVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEFA. FR 25	300
HESRQ       HESRQ	Qy 300 KTPDYEL 306          	
Qy 120 ITQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDTLDHIRA 179	RESULT 10 US-10-424-599-163708 ; Sequence 163708, Application US/10424599 ; Publication No. US20040031072A1	

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AL 180 :| SL 178 'RK 300 || 'RK 298

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Acvalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53228)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 333776
LENGTH: 208
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                                                                                                                                                                        241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAF
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                                                                                                                                               1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPV7
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; OTHER INFORMATION: Clone ID: ARATH-23APR03-C8015_1.p
US-10-739-930-6733
                                                                 Query Match

89.0%; Score 1486; DB 5;
Best Local Similarity 88.2%; Pred. No. 1.4e-146;
Matches 270; Conservative 16; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_67515C.1.pep
US-10-425-115-333776
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88.8%; Score 1483; DB 4

Best Local Similarity 87.0%; Pred. No. 3e-146;

Matches 268; Conservative 24; Mismatches 1
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OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 333776, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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ORGANISM: Zea mays
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LOCATION: (1)..(3
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          APPLICANT: La Royal Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION WIMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 163708
LENGTH: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6733, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_118848C.1.pep
US-10-424-599-163708
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NAME/KEY: unsure
LOCATION: (1)..(307)
OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Glycine max
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Matches 272; Conserv
      GENERAL INFORMATION:
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NAME/KEY: unsure
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APPLICANT: Shizuko Ishii
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Ai Wakamatsu
APPLICANT: Ai Wakamatsu
APPLICANT: Ai Wakamatsu
APPLICANT: Ai Wakamatsu
APPLICANT: Reisichi Nogai
APPLICANT: Tetsuji Ocsuki
APPLICANT: Chiaki Senoo
APPLICANT: Chiaki Senoo
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT PAPLICATION NUMBER: US 60/159, 590
PRIOR APPLICATION NUMBER: US 60/159, 590
PRIOR PLIANG DATE: 1999-10-18
PRIOR PLIANG DATE: 2000-02-17
PRIOR PLIANG DATE: 2000-02-17
PRIOR PLIANG DATE: 2000-02-17
PRIOR PLIANG DATE: 2000-01-11
PRIOR PLIANG DATE: 2000-05-02
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Query Match 85.4%; Score 1427; DB 4; Length 309; Best Local Similarity 83.7%; Pred. No. 2.2e-140; Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps
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<sup>129</sup> FYDECLRKYGNANVWKYFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHIRALDRLQE 188 186 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLVMEGY 245

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<sup>309</sup> L 309

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US-111-058-727-22
US-111-058-727-23

ALIGNMENTS

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APPLICANT: Yelsuo nibilikawa
APPLICANT: Koji Hayabhi
APPLICANT: Kaoru Otsuka
APPLICANT: Kaoru Otsuka
APPLICANT: Jun-Ichi Yamamoto
APPLICANT: Jun-Ichi Yamamoto
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Jun-Ichi Nogai
APPLICANT: Jun-Ichi Nezu
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APPLICANT: Jun-Ichi Nezu
APPLICANT: Jun-Ichi Nezu
APPLICANT: Jun-Ichi Nezu
TITLE OF INVENTION: PHOSPRATABE
FILE REFERENCE: 06501-099002
TITLE OF INVENTION: NUMBER: US/11/060,065
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 1999-07-29
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Publication No. US20050250144A1
GENERAL INFORMATION:
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APPLICANT: Takao Isogai
PPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
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CRGANISM: Homo sapiens
US-11-109-156-24
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370, App
370, Appl
6940, Ap
52, Appl
84, Appl
1246, Ap
2554, Ap
2554, Ap
256, Ap
256, Ap
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Sequence 39, Appl
Sequence 38, Appl
Sequence 184, App
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2502, Ap
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2: (2012 6) prodate 3/pubpaa/1809 NEW PUB. pep: *
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                  GenCore version 5.1.6
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTE
TITLE OF INVENTION: PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT APPLICATION UNMER: US/11/109,156
CURRENT APPLICATION NUMBER: US/11/060,065
PRIOR PEDICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2000-01-29
PRIOR PELING DATE: 2000-01-29
PRIOR PELING DATE: 2000-01-29
PRIOR PELING DATE: 2000-01-29
PRIOR PELING DATE: 2000-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ai Wakamatsu
Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jun-Ichi Yamamoto
Shizuko Ishii
Tomoyasu Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetsuo Nishikawa
                                                                                                    Query Match
Best Local Similarity 83.74
Matches 252; Conservative
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Jun-Ichi Nezu
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APPLICANT: Takao Isogai
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Kaoru Otsuka
                             ORGANISM: Homo sapiens
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US-11-109-156-39
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                                                                                                                                                                                                                                                                                                                                               245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 NWCQDKNVVTVPSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAPRQSEPDVTRKTPDYF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 NWCHDRNVVTIFSAPNYCYRCGNQAAIMELDDTLKYSFLQFDPAPRRGEPHVTRRTPDYF 308
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                                                                                                                                  9 ELDQWIEQIANECKQISESQVKSLCEKAKEILITKESNVQEVRCPVTVCGDVHGQPHDLMEL
                                                                                                       6 DVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHGQFHDLIEL
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                                                      Gaps
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APPLICANT: Chiark Sence
APPLICANT: Chiark Sence
APPLICANT: Jun-Ichi Nezu
TITLE OF INVENTION: NOYEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: NOYEL GENES ENCODING PROTEIN KINASE/PROTEIN
CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2002-01-29
PRIOR PLILING DATE: 2002-01-29
PRIOR PLILING DATE: 2000-07-28
PRIOR PLILING DATE: 2000-07-28
PRIOR PLILING DATE: 1999-10-18
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85.4%; Score 1427; DB 7; Length 309; 83.7%; Pred. No. 4.8e-132; ive 32; Mismatches 17; Indels
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Publication No. US20050250144A1
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Tetsuji Otsuki
Shin-Ichi Funahashi
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APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
APPLICANT: Koji Hayashi
APPLICANT: Moru Otsuka
APPLICANT: Shizuko Ishi
APPLICANT: Shizuko Ishi
APPLICANT: Tomoyasu Sugiyama
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Shizuko Ishii
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Ai Wakamatsu
                                                      Matches 252; Conservative
                           Similarity
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QY   178 RALDRIQEVPHEGPMCDLLWSDPD-DRCGWGISPRGAGYTFGQDIAEQFN		## APPLICANT: TOSAIO OCA ## APPLICANT: TOSAIO OCA ## APPLICANT: Teteno Nishikawa ## APPLICANT: Koji Hayashi ## APPLICANT: Koji Hayashi ## APPLICANT: Koji Hayashi ## APPLICANT: Shizuko Ishii ## APPLICANT: Shizuko Ishii ## APPLICANT: Ai Wahamantani	APPLICANT: Keiichi Nagai APPLICANT: Tetauji Otsuki APPLICANT: Tetauji Otsuki APPLICANT: Chiaki Senoo APPLICANT: Jun-Ichi Punahashi APPLICANT: Jun-Ichi Nezu TITLE OF INVENTION: NOYEL GENES ENCODING PROTEIN KINASE/PROTE TITLE OF INVENTION: PHOSPHATASE FILE REFERENCE: 06501-099002	NT APPLICATION NT FILING DATE APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION NAME OF THE ORDER OF TH	PRIOR FILING DATE: 2000-05-02	Query Match Best Local Similarity 46.3%; Score 757; DB 7; Length 323; Batches 142; Conservative 66; Mismatches 87; Indels  Qy 6 DVDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKC
; NUMBER OF SEQ ID NOS: 43 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 38 ; LENGTH: 319 ; TYPE: PRT ; ORGANISM: Homo sapiens US-11-109-156-38 Query Match Bast Local Similarity 46.3%; Score 757; DB 7; Length 319; Matches 142; Conservative 66. Mismarches 87; Indele 12. Gane 6.	SECKPLSELEVKNLCDQARTILVEEWNVQPVKCPTVCGDIHG 57	QY         118 RQITQVYGFYDECLRRYGNANVWKYFTDLFDLFALIEHEIFCLHGGLSPSLDTLDHI 177           Db         124 ASINRIYGFYDECKRRY-NIKLWKTFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQSWEQI 182           QY         178 RALDRIQEVPHGGPWCDLLWSDPD-DRCGWGISPRGAGYTFGODIAEQFNHTNGLSLVAR 236           Db         183 RRIMRPTDVPDQGLLCDLLWSDPRDVLGWGENDRGVSFTFGAEVVARFLHKHDLDLICR 242	QY         23.7 AHQLVMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSFLQFEPAPRQSEPD 296           Db         24.3 AHQVVEDGYEFPAKRQLVTLFSAPNYCGEFDNAGAMMSVDFTLMCSFQILKFAEKK-KFN 301           QY         29.7 VTRK-TP 302           I	RESULT 4 US-10-878-556A-184 US-10-878-556A-184 Sequence 184, Application US/10878556A Publication No. US20050266399A1 GENERAL INFORMATION: TITLE OF INVENTION: HCV regulated protein expression FILE REFERENCE 2.1762 CURRENT APPLICATION NUMBER: US/10/878,556A CURRENT FILING DATE: 2004-06-28 NUMBER OF SEQ ID NOS: 199 SOFTWARE: Patentin version 3.1 SEQ ID NO 184 LENGTH: 323	; TYPE: PRT ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; PUBLICATION INFORMATION: ; DATABASE ACCESSION NUMBER: sw_hum/pplg_human ; DATABASE ENTRY DATE: 1994-06-01 US-10-878-556A-184  Query Match  Query Match  45.3%; Score 757; DB 6; Length 323; Best Local Similarity 46.3%; Pred. No. 9.7e-67; Matches 142; Conservative 66; Mismatches 87; Indels 12; Gaps 6;	OY 6 DVDROIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDIHG 57

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HG 57 || HG 67 (ES 117 | | |EC 127

80 116	Db 175 YDACMDAFDCLPLALIALIERERC 175 YDACMDAFDCLPLAALMNQQFLC	Qy 200 PDDRCGWGISPRGAG   :   :   :   :   Db 235 PLEDFGNEKTQEHFTHNTVRGCS	Qy 252DVVTVFSAENYCYRCGN ::: :	RESULT 7  US-10-467-657-2502  Sequence 2502, Application US/10467  Publication No. US20050260581A1  GENERAL INFORMATION:  APPLICANT: CHIRON SpA  APPLICANT: PIZZA Mariagrazia  APPLICANT: PIZZA Mariagrazia  APPLICANT: MASIGNANI Vega  TITLE OF INVENTION: GONOCOCCAL PRO  CURRENT PILLING DATE: 2003-08-11  PRIOR PILLING DATE: 2001-02-12  CURRENT PILLING DATE: 2001-02-12  NUMBER OF SEQ ID NOS: 9218  SOFTWARE: SeqWin99, version 1.04  SOFTWARE: SeqWin99, version 1.04  SOFTWARE: SeqWin99, version 1.04  CUBCTH: 276  TYPE: PRT  CORGANISM: Neisseria gonorrhoeae  US-10-467-657-2502  QUETY MATCH  MATCHES 15 Millarity 25.0%; Pre  Matches 52; CONSETALGATION  OY SIGNIBLATION  OY GDIOGEOPELTALLGATION  OY GDIOGEOPELTALLGATION  OY GDIOGEOPELTALLGATION  OY 171 LDTLDHIRALDRIGEVPHECEPMC  OY 171 LDTLDHIRALDRIGEVPHECEPMC  OY 231 LSLVARAHQLVMEGYNWCQDRAV  OY 231 LSLVARAHQLVMEGYNWCGDRAV  OY 231 LSLVARAHQLVMEGYNWCQDRAV  OY 231 LSLVARAHQLVMEGYNWCGNONOND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HEREFERRORE: GDEGOUS CONDOUND  HER	
118 ROITQVYGFYDECLKKYGNANVWKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDTLDHI 128 ASINRIYGFYDECKRRY-NIKLWKTFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQSMEQI 170 DAIDDIOWDHECDMCHIEGEDDLDFCGMTEDDAGAGYTECCHIAFDRHIMMTESTSTAB		Qy 23.7 AHQLVMEGYNWCQDKNVVTVFSAPNYCYRCGNWAAIMEIDETWNRSFLQFEPAPRQSEPD 296  [  : : : : : ::: :: :: :: :: :: ::: ::	Qy 297 VTRK-TP 302          Db 306 ATRPVTP 312	PREDIGATION OF USE OF 34  PUBLICATION OF USE OF 34  PUBLICATION OF USE OF 34  PUBLICATION OF USE OF 34  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: TO AND I CESULA  APPLICANT: CALCAI NUMBER: US AND I CESULA  APPLICANT: CALCAI OF USE OF US	

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qq	:	
ò	140 WKYFTDLFDYLPLTALIEHEIFCLHGGLSPSLDTLDHIRALDRIQEVPHER	3D 199
q	175 YDACMDAFDCLPLAALMNQQFLCVHGGLSPEINTLDDIRKLDRFKEPPAY	1   3D 234
δ	200 PDDRCGWGISPRGAGYTFGQDIAEGFNHTNGLSLVARAHQLVI	JK 251
යු	235 PLEDFGNEKTQEHFTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRAHEAQ)	(S 294
δλ	252NVVTVFSAPNYCYRCGNMAAIMEIDETWNRSFLQFEPAP 290	
d	295 QTTGFPSLITIFSAPNYLDVYNNKAAVLKYENNV-MNIRQFNCSP 338	
RESULT US-10-	SULT 7 10-467-657-2502	
S	Sequence 2502, Application US/10467657 Publication No. US20050260581A1	
	APPLICANT: CHIRON SPA	
	APPLICANT: FONTANA Maria Rita APPLICANT: PIZZA Mariagrazia	
	L PROTEINS	
	S/10/46 -11	
	PRIOR APPLICATION NUMBER: GB-0103424.8 PRIOR FILING DATE: 2001-02-12	
	HBER OF SEQ ID NC TWARE: Segwin99,	
SE	SEQ ID NO 2502 LENGTH: 276	
; ; US-1	TYPE: PRT ORGANISM: Neisseria gonorrhoeae -10-467-657-2502	
no a	atc.	
Ma	SINITALLY 23.0%; FICH. NO. 52; Conservative 22; Mismatch	3 10;
δλ	53 GDIHGOFHDLIELF-RIG-GKAPDTNYLFMGDYVDRGYYSVETVSLLVAL)	FI 110
qa	7 GDIQGCFDELTALLGKIGFNHGTDTLWL-TGDIVNRGPKSLETLQFC	) 1 61
ò	111 LRGNHESRQITQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHEI:	95 170
qa	62 VLGNHDVILLAV	.5 83 .5 83
ολ	171 LDTLDHIRALDRIQEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQD	4G 230
qq	84 -DTIEPILKHPDGGKMLDWLRAQPLLIREGGRVMIHAG	126
ò	231 LSLVARAHQLVMEGYNWCQDKNVVTVFS 258	
qq	-Z	
RESU US-1	RESULT 8 US-11-135-855-41 Sequence 41, Application US/11135855	
	SENERAL INFORMATION: APPLICANT: SMITHKLINE BEECHAM ORPORATION APPLICANT: SMITHKLINE REFERMA D. 1.	
	TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GPSOID: FILE REFERENCE: GPSOID: FILE REFERENCE: GPSOID: FILE REFERENCE: GPSOID: FILE REFERENCE: GPSOID: FILE FILE FILE FILE FILE FILE FILE FILE	

EV 178
-G 135
KD 222
SP 169
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SP 277

Db 127 BRHIEVINKMNVPIVIVGQQHEQLHSIVHDDYKAGQIIGEWI Qy 94 VSLLVALKVRYRBRITILRGNHESRQITQVYGFYDECLRKY Db 179 FSVSEKDIAVGHRKRGLLDQ-LAKYQIKPNIHET QY 136 NANV	US-11-029-003-8  Sequence 8, Application US/11029003  Sequence 8, Application US/11029003  Sequence 8, Application US/11029003  Seneral Information. USO050260194A1  APPLICANT: BETERS, BADMREL 5.  APPLICANT: BETERS, DADM R.  APPLICANT: BITONII. ALAN J.  APPLICANT: BITONII. ALAN J.  APPLICANT: BITONII. ALAN J.  APPLICANT: BITONII. ALAN J.  APPLICANT: BITONII. ALAN J.  PRIOR RELIGATION NUMBER: US/11/029,003  CURRENT PRILING DATE: 2005-01-05  PRIOR PILING DATE: 2003-07-17  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR PILING DATE: 2003-09  PRIOR	309 INKYNHDIALLELDEPLVLNSYVTPIC 97 LVALKVRYRDRITILR 369 LQYLRVPLVDRATCLRSTKFTIXNNMF 126FYDECLRKYG-NANVWKYFTDLR 126FYDECLRKYG-NANVWKYFTDLR 129 ISWGEBCAMKGKYGIYTKVSRYVNWIK 169 PSLDTLDHIRALDRIQEVPHE 169 VFLFPFKPKDTLMISRTPEV 220 DIAEQFNHT-NGLSLVARA 532 EVHNAKTKPREEQKNSTYRVSVLTVL
CURRENT FILING DATE: 2005-05-24  PRIOR FILING DATE: 2005-08-13  PRIOR FILING DATE: 2002-08-13  PRIOR PLING DATE: 2001-02-14  PRIOR PLING DATE: 2001-02-14  PRIOR FILING DATE: 2001-02-14  PRIOR FILING DATE: 2000-02-14  PRIOR PLING DATE: 2000-02-29  NUMBER OF SEQ ID NOS: 46  SEQ ID NO 41  LENGTH: 250  TYPE: RATE  ORGANISM: Homo sapiens  US-11-135-855-41	Query Match Best Local Similarity 22.1%; Score 87; DB 7; Length 250; Best Local Similarity 22.1%; Pred. No. 0.13; Matches 49; Conservative 29; Mismatches 80; Indels 64; Gaps 11;  QY 111 LRGHESROITOVECKEYPECLAKYCRAAAHLDVEPLALIEHEIPCLHG 165 : Calsell Similarity 22.1%; Pred. No. 0.13;  QY 166 GLSPSLDTLDHIRALDRICENFURDARAHLDVSPLNFSLFHC 79  QY 166 GLSPSLDTLDHIRALDRICEVPHEGPMCDLLWSDPDDRCGWGISPRGAGYPFGQD 220	NUMBER OF SEQ ID NOS: 424

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-- 125 GI 428 .LS 168 :PS 488 GQ 219 GV 531 GN 268 SN 574

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SOFTWARE: FastSEQ for Windows Version 4.0
                  SEQ ID NO 52
LENGTH: 677
TYPE: PRT
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APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Ralbert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: Billy Fred McCutchen
APPLICANT: James F. H. Wong
APPLICANT: James F. H. Wong
APPLICANT: James F. H. Wong
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35118/287809
FILE REFERENCE: 35118/287809
CURRENT APPLICATION NUMBER: 60/391,786
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR APPLICATION NUMBER: 60/460,787
FRIOR APPLICATION NUMBER: 10/606,320
FRIOR FILING DATE: 2003-04-04
FRIOR FILING DATE: 2003-06-25
FRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
                                                                                                                                                           Sequence 6440, Application US/10467657

Publication No. US20050260581A1

GENERAL INPORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FOUTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MONACI Eliaabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE: 2003-08-11

PRIOR APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEQ ID NOS: 9218

SOFTWARE: SEQ ID NOS: 9218

SEQ ID NO 6540

LENGTH: 264
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4.6%; Score 76; DB 6; Length 264;
Best Local Similarity 22.5%; Pred. No. 1.7;
Matches 36; Conservative 18; Mismatches 60; Indels
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                                               Sequence 52, Application US/11058727
Publication No. US20050261483A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6940
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GRUEKALL INFORMATION:

APPLICANT: Ronald D. Flannagan

APPLICANT: Refael Herrmann

APPLICANT: Refael Herrmann

APPLICANT: Theodore W. Kahn

APPLICANT: Theodore W. Kahn

APPLICANT: James F. H. Wong

APPLICANT: James K. Presnail

APPLICANT: Gao-Guo Yu

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

FILE REFERENCE: 35718/287809

CURRENT APPLICANTON NUMBER: 06/331,786

PRIOR APPLICATION NUMBER: 60/331,786

PRIOR APPLICATION NUMBER: 60/460,787

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

PRIOR FILING DATE: 2003-04-04

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4.5%; Score 75.5; DB 7; Length 677
Best Local Similarity 17.4%; Pred. No. 6.4;
Matches 70; Conservative 63; Mismatches 128; Indels 1.
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, ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-52
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Publication No. US20050261483A1
GENERAL INFORMATION:
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AL 100

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RV 385 ET 278 FF 445

PR 211 SI 327

Qy 61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYS	238NYDROMKLTABYSDHCVKWYETGLAKLKC 152 LTALIEHEIFCLHGGLSPSLDTLDHIRALDRIQEVPHEGPMCI	Db 285 LAVLDVVALFPNYDTRTYPMETKAQLIREVYTDPL  Qy 212 GAGYTFGQDIAEQFNHTNGLSLVARA	241	DD 386 SKGSNLQQMYGINQNLHSISIFDFTNYDIYKTLSKDAVLLDIVYPGYTYI  Qy 279 MNRSFLQFEPAPRQSEPDVTRKTPDY 304                         Db 446 MVNOINNTRYTI,KYNPVSKDITASTRDSELELPPETSDDNY 487	SULT 15	1 . 0	•	; APPLICANT: Aller L. Lu ; APPLICANT: Billy Fred McCutchen ; APPLICANT: James K. Presnail ; APPLICANT: James F.H. Wong	; APPLICANT: Cao-Guo Yu ; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal ; TITLE OF INVENTION: Activity	REFERENCE: 357 VT APPLICATION VT FILING DATE APPLICATION	; PRIOR FILING DATE: 2002-06-26 ; PRLOR APPLICATION NUMBER: 60/460,787 ; PRIOR FILING DATE: 2003-04-04 ; PRIOR PAPI-ICATION NUMBER: 10/606.320	; PRIOR FILING DATE: 2003-06-25 ; NUMBER OF SEQ ID NOS: 134 ; SOFTWARE: FastSEQ for Windows Version 4.0	; SEQ 1D NO 84 ; LENGTH: 677 ; TYPE: PRT ; ORGANISM: Bacillus thuringiensis	Query Match Query Match Best Local Similarity 17.4%; Pred. No. 6.4; Matches 70; Conservative 63; Mismatches 128; Indels 1	Qy 7 VDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCG	61 61 61 61	101
Query Match 4.5%; Score 75.5; DB 7; Length 677;  Best Local Similarity 17.4%; Pred. No. 6.4;  Matches 70; Conservative 63; Mismatches 128; Indels 141; Gaps 18;  Qy 7 VDRQISBCEREVENEDRANTILVERWNVOPVKCPVIVCGDIHGOFH 60	Db 123 INQKİABYARNKALSELEGLGNNYQLYLTALEEWEENPFRSRGSINGSRPALRIVRNRFE 182  Qy 61 DLIELFRIGGKAPDTNYLEMGDYUDRGYYSVETVSLLVAL 100  Db 183 ILDSLFTQYMPSFRVTNFEVPFLTVYAMAANLHLLLIKDASIFGEEWGWSTTTIN 237	101	QY 152 LTALIEHEIFCLHGGLSPSLDTLDHIRALDRIQEVPHEGPMCDLLWSDPDDRCGWGISPR 211	OY 212 GAGYTPGQDIAEQFNHTNGLSLVARA	Qy 241UMEGYNWCQDKNVTVFSAPNY-CYRCGNMAAIMEIDET 278 :	QY 279 MNRSFLQFEPAPRQSEPDVTRKTPDY 304	RESULT 14 US-11-108-389-52	; sequence 32, Application US/III08389 ; Publication No. US20050261188A1 ; GENERAL INPORMATION: ; APPLICANT: Andre R. Abad	; APPLICANT: Ronald D. Flannagan ; APPLICANT: Rafael Herrmann ; APPLICANT: Theodore W. Kahn	<pre>; APPLICANT: Albert L. Ld ; APPLICANT: Billy Fred McCutchen ; APPLICANT: James K. Presnail ; APPLICANT: James F.H. Wong</pre>	<pre>; APPLICANT: Cao-Guo Yu ; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal ; TITLE OF INVENTION: Activity : FILE REFERENCE: 35718/291049</pre>	CURRENT APPLICATION NUMBER: US/11/108,389 CURRENT FILING DATE: 2005-04-18 PRIOR APPLICATION NUMBER: 60/391,786	; FRIOR FILING DATE: 2002-06-26; PRIOR APPLICATION NUMBER: 60/460,787; PRIOR FILING DATE: 2003-04-04 ; PRIOR FILING DATE: 10/606,320 ; PRIOR APPLICATION NUMBER: 10/606,320	NUMBER OF SEQ ID NOS: 134 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 677	; TYPE: PRT ; ORGANISM: Bacillus thuringiensis (mutated) US-11-108-389-52	Query Match 4.5%; Score 75.5; DB 7; Length 677; Best Local Similarity 17.4%; Pred. No. 6.4; Matches 70; Conservative 63; Mismatches 128; Indels 141; Gaps 18;	Qy 7 VDRQIEQLSECKPLSELEVKNLCDQARTILVEEWNVQPVKCPVTVCGDİHGQFH 60 ::::  :

-- 237 LP 151

FH 60 | FE 182

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NYYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQWVDYNQFRREMT 284	152 LTALIEHEIFCLHGGLSPSLDTLDHIRALDRIQEVPHEGPMCDLLMSDPDDRCGWGISPR 211	285 LAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSI 327	212 GAGYTFGQDIAEQ FNHTNGLSLVARAHQL 240		241VWEGYNWCQDKNVVTVFSAPNY-CYRCGNMAAIMEIDET 278	386 SRGSNLQQMYGTNQNLHSTSTFDFTNYDIYKTLSKDAVLLDIVYPGYTYIFFGMPEVEFF 445	279 MNRSFLOPEPAPROSEPDVTRKTPDY 304	446 WUNQLANVTRKTLKYNPVSKDIIASTRDSELELPPETSDQPNY 487
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/product= "PP2A-4"
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                                           Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Cgn2_1/USF70 = Spool_p/US10764259/runat_05122005_094547_7008/app_query.fasta_1.455
-DB=N Geneseq -QFNT=fastap -SUFFIX=p2n.rng -NINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNTRYT=pto -NORM=ext -HEAPSIXE=50 -MINIMATCH=0 -MAXIEN=200000000
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-NO NMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBEOCK=100 -LONGLOG
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                   - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                      4996997 seqs, 3332346308 residues
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Plant; ss; gene; PP2A-4; protein phosphatase; PHSRP; cold; phosphatase stress related protein; environmental stress; d: salt tolerance.
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/product= "PP2A-4"
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VAN THIELEN N.
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(BOHM/) BOHNERT H J.
(VTHI/) VAN THIELEN I
(CHEN/) CHEN R.
(ISHI/) ISHITANI M.
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                                                                                                                                                                                                                                                                                                                                   The invention relates to a transgenic plant cell (I) transformed by a phosphatase stress-related protein (PHSRP) coding nucleic acid (ABN81330-ABN81334), where expression of the nucleic acid in the plant cell results in increased tolerance to an environmental stress as compared to a wild type variety of the plant cell. PHSRP encoding genes are useful for identifying Physcomitrella patens and related organisms, as markers for specific regions of the genome, mapping of genomes of organisms related to P. patens, identification and localisation of P. patens sequences of interest, evolutionary studies, determination of PHSRP regions required for function, modulation of a PHSRP activity, modulation of the metabolism of one or more cell functions, modulation of stress resistance. The gene is also useful for identifying and/or cloning PHSRP homologues in other cell types and organisms, for identifying an organism as being PHSRP studies. The present sequence is that of a PHSRP encoding
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                                                                                                                                                                                New transgenic plant cell transformed by phosphatase stress-related protein coding nucleic acid whose expression in the cell results in increased tolerance to environmental stress compared to wild type cell.
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The invention relates to a transgenic plant cell transformed by a phosphatase Stress-Related Protein (PHSRP) coding nucleic acid. The expression of the nucleic acid in the plant cell results in increased tolerance to an environmental stress (e.g. salt tolerance, cold and drought) as compared to a wild type variety of the plant cell. Also include are a transgenic plant comprising the novel plant cell. Also produced by the transgenic plant comprising the novel plant cell, a seed produced by the transgenic plant of (where the seed is true breeding for an increased tolerance to environmental stress as compared to a wild type variety of the plant cell, an agricultural product produced by the plant or seed, an isolated PHSRP or PHSRP coding nucleic acid, and producing a transgenic plant of plant containing PHSRP nucleic acid. The transgenic plant cell transformed by a Phosphatase Stress-Related Protein (PHSRP) coding nucleic acid is useful for modifying stress tolerance of a plant. The present sequence encodes the PHSRP, protein phosphatase, PP2A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp
               New transgenic plant cell transformed by a Phosphatase Stress-Related
Protein (PHSRP) coding nucleic acid, useful for modifying stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspleulleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet
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Matches:
Conservative:
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Indels:
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                                                                           Claim 18; Fig 2C; 79pp; English
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1670.00
100.00%
100.00%
                                              tolerance of a plant.
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Aspàrg11eG1nG1uVa1ProHisG1uG1yProMetCygàspLeuLeuTrpSeràspPro 200

551 181

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q <sub>0</sub>	611 GATCGTATTCAAGAAGTGCCGCACGAGGGCCCGGATGTGTGATCTACTCTG	CA 670
ò	201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPh	.sp 220
qg	671 GATGATCGTTGTGGGGCATTTCACCACGAGGTGCCGGTTATACTTT	AT 730
ò	221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl	eu 240
q	731 ATTGCAGAGCAGTTCAATCATCAATGGTCTAAGTTTGGTTGCACGTGC	TT 790
8 8	241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh	ro 260
<u> </u>		
충 음	261 ASTTYTCYSTYTATGCYSG1yASTMELN1AAA11EMECG1UI1EASDG1 	sn 280 
ò	281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa	ув 300
q	911 CGGTCTTTTCTTCAGTTCGAACCAGCACCGCGGCAAAGTGAACCAGATGT	 AG 970
ò	ThrProAspTyrPheLeu 30	;
<b>q</b> q	971 ACTCCTGATTACTTTCTG 988	
RESULT ACC433 ID A	ULT 3 43349 ACC43349 standard; cDNA; 1386 BP.	
A XX	ACC43349;	
X E	11-AUG-2003 (first entry)	
X B I	Protein phosphatase stress-related polypeptide GmPP2A-5 cDN	
X X	tress-related polypeptide; PPSRP; PpP	PP-1;
<b>3 2 3</b>	BnPP2A-1; BnPP2A-2; BnPP2A-3; CmPP2A-1; CmPP2A-2; CmPP2A-3; OSPP2A-2; OSPP2A-3; plant tolerance; environmental stress; drought. salinity. And. environmental stress;	1,
<b>X</b> 8	Control of the contro	
8 <b>X</b>	GIYCLIIC MAX.	
FF	Key Location/Qualifiers CDS 921012	
L	/*tag= / /www.hate = monetois showshates at sec.	
E	/product= "protein phospharase stress-relat polypeptide"	
¥ &	WO2003020914-A2.	
X & :	13-MAR-2003.	
X & I	05-SEP-2002; 2002WO-US028445.	
X & I	05-SEP-2001; 2001US-0317305P.	
X &	(BADI ) BASF PLANT SCI GMBH.	
X II X	Bohnert HJ, Chen R, Ishitani M, Van Thielen N, Da Costa	0.
\$ 8 8 i	WPI; 2003-300886/29. P-FSDB; ABP98034.	
XLLL	New protein phosphatase stress-related polypeptide coding n useful for modulating plant's tolerance to an environmental as drought, increased salinity and cold.	cid, such
XX PS	Claim 1; Page 82; 107pp; English.	
XSS	The present sequence encodes a protein phosphatase stress-r nolvmentide (PPSRP). The specification describes PPSRP nolv	
: 당	PpPP-1, BnPP2A-1,	

241	!	812	261	872	281	932	301	992	RESULT 4 ACC43354 ID ACC43354	ACC43354;		Protein p Protein p Brobola-1.	OSPP2A-2; drought;	Oryza sat	Key CDS		WO2003020	13-MAR-20	05-SEP-20	05-SEP-20 (BADI ) B	Bohnert H	WPI; 2003 P-PSDB; A	New prote useful fo	as drougn Claim 1;	The prese	polypepti designate GmPP2A-2,	Physcomit polypepti	tolerance salinity	Oryza sat related t	function,
-	Ž	qa	<del>ک</del>	qu	δ	qa	oy.	q <sub>0</sub>	RESULT ACC433 ID A	XX VX		Z X X	KW	XX SS	Y E E	FF	E XX	X 8 X	XX	PR XX	XX II XX	9.0 P.	XX PT	XX SS	¥8 ¥8	888	ខ្លួ	888		-
		polypeptides and polynucleotides are useful for modulating plant tolerance to an environmental stress such as drought or increased		Orygan Satisfaction of and the mapping of genomes of organisms	related to the above bleates, in a evolutionary and polypeptide structural studies, in determination of PPSRP regions required for function modulation of modulation of manual structures.	or more cell functions and transmembrane transport of one or more	XX XX SQ Sequence 1386 BP; 368 A; 273 C; 338 G; 407 T; 0 U; 0 Other;		5.95e-166 1549.00 96.73%	Mismatches: Indels: Gans:	10-764-259-13 (1-306) x ACC43349 (1-1386)	Qy         1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu         20	21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThr1leLeuValGluGluTrp		41 AsnvalGlnProvalLysCysProvalThrValCysGlyAspIleHisGlyGlnPheHis	212 AACGTGCAACCGGTTAAGTGCCCCCGTCACCGTCTGCGGCGATATTCACGGCCAGTTCTAC	OY 6.4 ASPERTANCE THE OFFICE O	81	332 GGTGATTATGTAGATCGTGGATACTATTCAGTGGAGACTGTTACACTTTTGGTGGCTTTG	<pre>Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAshHisGluSerArgGlnIle 120                                      </pre>	Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140	Db 452 ACTCAAGTGTATGGCTTCTATGATGCTTGAGAAATATGGAAATGCGAATGTCTGG 511	OY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160	161	Db 572 TTCTGCTTGCATGGAGGTCTCTCTCTTTGGATACACTGGATAACATCAGAGCATTG 631	Qy         181 AspArg11eG1nG1uVa1ProHisG1uG1yProMetCysAspLeuLeuTrpSerAspPro 200	Qy 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220	DD 692 GATGATGGCTGTGGGAGAATATCTCCACGTGGTGCAGGATACACATTTGGGCAGGAT 751	Qy 221 IlealaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240	

ò qa	241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh. 	70 260       3871
ò	261 ASHTYLCYSTYTATGCYSG1yASHMetAlaAla1leWetGlulleAspG1)	3n 280
g &	872 AATTACTGTTATCGATGTGGGAATATGTGGCTGCCATACTAGAAATAGGAAGA 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa	YT. 931
ପ୍	932 CAGRATITICITCAGITIGATCCAGGTCCCAGGCAAAITGAGCCTGACGC	) 3G 991
δδ	301 ThrProAspTyrPheLeu 306	
qa	992 ACTCCAGATTATTTTG 1009	
RESULT ACC433 ID A	RESULT 4 ACC43354 ID ACC43354 standard, cDNA; 1330 BP.	
× ××	ACC43354;	
[ ]	11-AUG-2003 (first entry)	
E B X	Protein phosphatase stress-related polypeptide OsPP2A-5 CDN	
<b>*</b>	Protein phosphatase stress-related polypeptide; PPSRP; PpPP: BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3; OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress; j drought; salinity; cold; enzyme; gene; ss.	2P-1; 1;
×83	Oryza sativa.	
XX H I I I I I I I I I I I I I I I I I I I	Key Location/Qualifiers CDS 1041024 /*tag= a /product= "protein phosphatase stress-relation phosphatase stress-relation phosphatase stress-relation phosphatase stress-relation phosphatase stress-relation phosphatase stress-relation polypeotide"	
XX	WO2003020914-A2.	
X & I	13-MAR-2003.	
X 44 i	05-SEP-2002; 2002WO-US028445.	
X & !	05-SEP-2001; 2001US-0317305P.	
X & S	(BADI ) BASF PLANT SCI GMBH.	
Y I S	Bohnert HJ, Chen R, Ishitani M, Van Thielen N, Da Costa	3,1
¥ 8 8 1	WPI; 2003-300886/29. P-PSDB; ABP98039.	
X E E E	New protein phosphatase stress-related polypeptide coding nuseful for modulating plant's tolerance to an environmental as drought, increased salinity and cold.	sid, such
X 23 3	Claim 1; Page 87-88; 107pp; English.	
1888	The present sequence encodes a protein phosphatase stress-ripolypeptide (PPSRP). The specification describes PPSRP polypolationsted propolation phopolation perpolations and propolation propolations.	
888	GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived Physcomitrella patens, Brassica napus, Glycine max or Oryza	PPSRP
888	polypeptides and polynucleotides are useful for modulating   tolerance to an environmental stress such as drought or inc.	
388	Ballinty and cold. Hey are also ustent in tremitation of localization of Physcomitrella patens, Trassica napus, Glyc: Oryza sativa and related organisms, mapping of genomes of o	or
888 	related to the above species, in a evolutionary and polypepi structural studies, in determination of PPSRP regions requi- function, modulation of PPSRP activity, modulation of metab	one

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	260 PR 01-UIN-1 BR 03-UIN-1 PR 03-UIN-1 PR 04-UIN-1	260 PR 03-UIN-1 883 PR 03-UIN-1 280 PR 04-UIN-1 280 PR 07-UIN-1 943 PR 10-UIN-1 943 PR 10-UIN-1

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The invention describes a recombinant DNA construct compris:

C polymucleotide consisting of a sequence encoding an amino a available in electronic form from the US patent office at ftp. seqdate.uspto.gov/sequence.html?DocID:2004034888. The poof of the invention are also useful in physical arrays of molect plant breeding markers. The recombinant DNA construct is use improving plant tolerance to cold, heat, drought, herbicides osmotic conditions, pathogens or pests, for manipulating green plant cells by modification of the cell cycle pathway. For a increased resistence to plant disease, for producing galactic lignin or plant growth regulators, for increasing the rate of computation in plants, for improving yield by modification photosynthesis or carbohydrate, nitrogen or phosphorus use or by providing improved plant growth and development under stress condition or for modifying seed oil or protein yield content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA consi
                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct, useful for improving plant to cold, heat, drought, herbicides, extreme osmotic conditions pests, for conferring increased resistance to plant disease
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05-NOV-2001; 2001US-00985678.
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270 AATGTTCAGCCGGTTAAGTGTCCCGGTCACCGTCTGCGGCGACATCCACGGCCAGTTTTAC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; pest tolerance; galactormannan production; lignin production; plant growth regulator; yield; plant growth, plant development; seed oil; protein yield; protein content; gene; ss.
                                                           GATCTGATTGAGCTTTTTAAGATCGGTGGTTCTTCGCCTGACACCAATTATCTCTTCATG
                                                                                                               GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu
                                                                                                                                     GGCGATTACGTAGATCGAGGGTATTATTCTGTGGAGACAGTCTCGCTCTTGGTAGCACTC
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                                     AspleulleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet
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                        PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu
                                                                                                                                                                                              Asparg11eGlnGluVa1ProHisGluGlyProMetCy8AspLeuLeuTrpSerAspPro
TTCTGCCTACATGGTGGTCTCTCTCCATCACTGGATACATTGGATAATATCGCGCCCTT
                                                                                                                                                                                                        AspaspargCysGlyTrpGly11eSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp
                                                                                                                                                                                                                                         GATGACCGATGTGGGTGGGGAATTTCACCAAGGGGTGCTGGATACACATTTGGCCAAGAT
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036	otein phosphatase stress-related ation describes PPSRP polypeptides 2A-1, BnPP2A-2, BnPP2A-3, GmPP2A-1, P2A-2 or OSP2A-3, derived from apus, Glycine max or Oryza sativa. Bes such as drought or increased information and inseful in identification and	6 6 6 6	0 ~ 0 ~ 0

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     CCAAACTACTGTTATCGCTGTGGTAACATGGCTGCAATTCTTGAGATTGGCGAAAACATG 1012
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41 ABNVAIGHDPROVAILYBCYSPROVAITHRVAICYGGIAVBPIILE 121 AANTSTTCAACCGGTTAAGTGTCCGGTTACGGTTATCGGGGATATC 61 ASPLEUII EGIULEUPHAATGITCGGGTTATGGTCCTCATAGT 81 GACCTAATTGAGCTATTTCGTATTGGTGGTAATGCTCCTGATAGT 82 GAGATTATGAGCTATTTCGTATTGGTGGTAATGCTCCTGATAGT 81 GIABPTYRVAIASPARGIGYTYTTGGTGTAATGCTCCTGATAGT 82 GAGATTATGAGATTGAGACTATTTCGTAGAACGTTCTTGAGAACGTTCTTGAGAACGTTCTTGAGAACGTTCTTATGAGAACGTTCTTAGAGATTGAGAACTTCTTATGAGAACGTTCTTAGAGAACATTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAACTTCTTAGAGAATTACAGAACTTTAAGAATTAGAAACAATTCTAGAAATTAGAAACAATACTTAGAAATTACAAAACAATACTTAGAAATTAGAAAAATAAAAAAAA	41 ASDVAIGHDFOVALLYSCYSPROVATHING	G 66	61		  AAGCTAAAGCG	ATTCTTGT	
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61 AspLeutleGluLeuPheArgileGlyGlyLysAlaProAspThr 181 GACCTAATGGGCTATTCGTATTGGTGTGATAGCTGCTGATAGT 81 GlyAppTrV4JAspArgGGTGTTTGTGGTGATAGCTGCTGATAGT 8241 GAGATTATGAGTCGTGGCTACTATTCTGTAGAAGGTCTCT 101 LysValArgTArGAATCGTGGCTACTATTCTGTAGAAACAGTCTTGT 101 LysValArgTyrArgaaATCGTGGCTACTATTCTGTAGAAACAGTCTTGT 101 LysValArgTyrArgaaATCGTGGCTACTATTCTGTAGAACAGTCTTGT 101 LysValArgTyrArgaaAACGTGTTAGGAATCCTGAGGAATCATTAGGAATCCTTAGGAATCCTTAGGAATCCTTAGGAATCCTTAGGAATCCTTAGGAATCCTTAGGAATCCTTAGGAATCCTTAGGAATCCTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTAGGAATCCTTTTAGTAGTTTATCATTAGTAGTTTTAGGATTATTCATTAGGATTATTCATTAGGATTATTCTCTTTAGGATTATTCTTAGGATTATTTAGTTAG	61 ASPLeuileGluLeuPheArgileGlyGlyLysAlaProAspThr 81 GACCTAATGAGGTATTGGTATTGGTAGTAGTGGTAGTGGTAGTGGTG	qq	121	AATGTTCAACCGGTTAA	ratgegegai	Arccarge	
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8   GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSer   1	81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSer [41] GGGATTATGTGGGCTACTATCTGTGGAGGCTTCTT [42] GGGATTATGTGAGTCGGTGCTTATCTGTGAGAGAGTCTCT [43] AGGTGCGTTACAGGGACTATCTGTGAGAGAGTCTCT [44] AGGTGCGTTACAGGACTTACGATCCTGCGAGGGAATCAT [45] AGGTGCGTTACAGGACTTACGATCCTGCGAGGGAATCAT [45] AGGTGCGTTATGATTTATGACGAATGCTTGAGGAATACGGA [47] AGGTATTTACGGACCTTTTATGACGAATGCTTGAGGAATACGGA [48] AGTATTTACGGACCTTTTTATGACGAATGCTTGAGGAATACGGACTCAGGACTTTACGATTATTACGGACTTTCACAGGACTTTACGATTATTACGGACTTTCACAGCATTACTTTCAGAGACTTTCAGAGACTTTCAGAGACTTTCAGAGACTTTCAGAGACTTTCAGAGACTTTCAGAGACTTTCAGAATACTTGAGAATACAAGAGACTTCACAGAATACTTCAGAATACTTGAGAATACTTTCAGAATACAGAGACTTACACAGAGACTTCACAGAATACTTCAGAATACTTTGAATACTTCAGAATACTTCAGAATACTTTGAATACTACAGAATACTCACTTGAGAATACTTTCAGAATACTTTCAGAATACTTTCAGAATACTTTCATTCA	qq	181		ATGCTCCTGAI	ACTAATTA	
241 GĠĠĠŦŦĀŦĠŦĠĠŦĠŦŢĠŢĠĠŦĠŢŦĠŦĀĠĀĀĠĠŢĠŢĠŢĠŢĠŢ	14.1 GGAGATTATGGAGATGGGGTACTATTGTAGAAACAGTCTCCCCCCAGAGAATCATCTCCCCCAGAGAATCATCTCCCCCAGAGAATCATCCCCCAGAGAATCATCATCCCCCAGAGAATCATCATCATCCCCCAGAGAATCATCATCATCATCATCATCATCATCATCATCATCATC	ò	81		alGluThrVal	Serbeube	
101 LysValArgTyrArgAspArg11eThrI1eLeuArgGlyAsnHisc	10.1 LysValArgTyrArgAspArg11eThrIleLeuArgGlyAsnHisc	qq	241		TAGAAACAGTC	TCTCTATI	
301 ÀÀGĠTĠGTTÄCĂĠĠĠAĞĀĠTTĀĊĠĂTĊTĠĊĠĠĠĠĂĀTĠTĠTĠŢŢŢŢĠŢŢŢĠŢŢĠŢŢĠĠŢŢŢĠĠŢŢŢĠĠŢŢ	11 ThrGlnValTyrGlyPheTyrAspGluCySLeuArgLysGAATCAGAATACAGAATTAGACGAATTATACAGACTTTTAGATTATTATATATA	<i>δ</i> ο	101		euArgGlyAsr	HisGluSe	
121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyR 361 ACACAGCTTATGGTTTTATGACGATGCTTGGGAATACGGAA 141 LysTyrPheThrAspLeuBheAspTyrLeuProLeuThrAlaLeu1 421 AACATTTTATGGATTTTTATGACGATGCTTGACGACTCTCGGATGCTTTACACACAC	1. ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGly	QQ	301		TGCGAGGGAAT	CATGAGAG	
361 ACM CANDER THE CONTROL OF THE CO	ACACATCTATGGTTTTTTTGATGGTTTTTTTTGATGGTTTTTTTT	ò	121		euArgLysTyr	GlyAsnAl	
141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeu 421 AAGTATTTTAGGGACCTTTTGATTATCTCCTTTACAGGACTC 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAsp 181 TTGTTTGATGGAGGAGGACCTTTCACTTCTCTTGGATACTTGGATACTTTGGATACTTTTGGATACTTTTTTTT	1. LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeu	qa	361		TGAGGAAATAC	GGAAATGC	
421 AGTATTTTACGGACCTTTTCGATTATCTCCCTCTTACAGCACTC  161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAsp  481 TTCTGTTTGCATGGAGGCCTTTCACCTTCTGGATACTCTTGAC  181 AsparglleGlnGluValProHisGluGlyProMetCySAspLeu  181 AsparglleGlnGluValProHisGluGlyProMetCySAspLeu  181 AsparglleGlnGluValProHisGluGlyProMetCySAspLeu  201 AsparglaCAGGAGGGTCCCCACGAGGACCAATGGCGATCTA  201 AsparglaCAGGATCCACCACGAAGGACCAATGGCGATCTA  201 AsparglaCAGGATCAGGATATCACACAGGACCAATGGCGATCTCA  201 AsparglaCAGGATCAGGAATATCATCACTCAGGATCTCAGGTTCTCA  21 IlealaGluGlnPheAsnHisThrAshGlyLeuSerLeuValAla  22 IlealaGluGlnPheAsnHisThrAshGaCTGAGTCTGATCTCA  23 IlealaGluGlnPheAsnTrACATAACAAAGGACTGAGTGATCTCA  24 ValMetGluGlyTyrAshTTAATCATAAAAAGGACTGAGTGTAAA  26 AshTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIle  72 GTAATGGAAGGCTATAATTGGTGCAGAAAAAAAAAGGATGGAGTAA  26 AshTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIle  78 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluPro  89 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluPro  1	21 AddritrinGGACCTTTCGATTATCCCTCTTACAGCACTC 61 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAsp 81 TTCTGTTTGCATGGACCTTTCACCTTCTCGGATACTCTTGAC 81 AsparglleGlnGluValProHisGluGlyProMetCysAspLeu 41 GATCGAATACAAGAGTTCCACACGAAGACCAATGTGCGATCTACACGATCTTCTCTGGATCTTTGATCTTGATCTTCTCTCTGGATCTTTTGATCTTGATCTTTTTTTT	δλ	141		roLeuThrAla	leulleGl	
161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAsp  481 TTCTGTTTGCATGGAGGCCTTTCACCTTCTCTGGATACTCTTGAC  181 AspArglleGlnGluValProHisGluGlyProMetCysAspLeu  [11	61 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAsp [11] [11] [11] [11] [11] [11] [11] [11	qq	0		CTCTTACAGCA	CTCATAGA	
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541 ĠATĠAAŢĀĊĀĀĢĠTŢĊĊĀĊĀĀĠĢĊĊĀĀŢĠĊĠĄŢŢŸ 201 ASPASPARGCYSGIYIPGIYILESETPROĀŢĠIŊĀJaGIYŢY 601 GACGATCGTTGGGATGCGGAATATCTCCTCGTGGTGGTTAC 221 IlealaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAla 61 IlealaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAla 61 ATGCTACTCAGTTAATCATAACAATGGACTGAGTCTGATCTCA 241 ValMetGluGlyTyrAsnTrGCGCAATGGACTGAGTCTCATCATCATCATCATCATCATCATCATCATCATCATC	41 GATCGAATACAGGGTTCCACACGAAGGACCAATGTGCGATCTA 01 ASPASDARGCTTCCACACGAAGGACCAATGTGCGATCTA 01 ASPASDARGCTTGAAGGTTCCACACGAAGGACCAATGTGCGATCTTA 01 GACGATCGTTGACAATGACAATACTCCTCGTGGTTGATTAC 11 IAAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValhla 12 IIealaGluGlyTyAsnTTCATAACATGGATGTGTGTTTTTTTT 14 ValMetGluGlyTyAsnTTCATAACAGAAAGACTGAGTTGTTTTTTTTTTTTTTTT	δλ	ω	Aspargi	SASI	LeuLeuT	
201 AspaspargCysGlyTrpGlylleSerProArgGlyAlaGlyTyr [	01 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyr	q Q	541	1 GATCGAA	CGA	TACTOT	
601 dacdarderregardeddararrerecregarderregraphe 221 IlealadludlnPheAsnHisThrAsnGlyLeuSerLeuvalAla 221 IlealadludlnPheAsnHisThrAsnGlyLeuSerLeuvalAla 661 ATTGCTACTCAGTTTAATCATAACAATGGACTGAGTCTGATCTCA 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThr 721 GTAATGGAAGGCTATAATTGGTGTCAGGAAAGAACGTAGTGACA 661 ASnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGlulle 721 GTAATGGAAGGCTATAATTGGTGTCAGGAAAGAACGTAGTGACA 671 ASTATCTATTAATGGTGTAAAAAAAAAAACAACTAGGAATTCTTGAGATT 781 AACTACTGTTAAAATTCGAATGCAGCAATTCTTGAGATT 781 CAGAACTTCCTTCAATTCGATCCAGCACCTAGACAAGCCC 301 ThrProAspTyrPheLeu 306 1	ol dacdarcerrecardegedararcrecrecrecrecrecrecrecrecrecrecrecrecre	λo	201	Aspaspa	rgGlyAlaGly	<u> ~</u>	
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261 AsnTyrCysTyrArgCysGlyAsnMetalaalaileMetGluileAs [	61 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaileMetGluileAs	Op	7		AGAACGTAGTG	ACAGTGTT	
781 ACTGGTTACGATGTGGAACATGGCCGCATTCTTGAGTTGG 281 AZGSEPPAELGUGINPHGGIDPACALAFCAGGCCGCAATTCTTGAGTTGG 281 AZGSEPPAELGUGINPHGGIDPACALAFCAGGCAGCTAGAGTCGAACCCGA 301 ThrProAspTyrPheLeu 306 301 ThrProAspTyrPheLeu 306 901 ACCCCTGATTTTTG 918	81 ACTACTOTTACATGIGATION  81 ACTACTOTTACATGIGATACATCOCCAATTCTTGIGATTCC  81 ACTACTOTTACAATGIGAAACATCOCCAATTCTTGIGATTCC  81 ACTACTOCTTCAATTCGATCCAACCTAGACAAGTCCAACCCGA  41 CAGAACTTCCTTCAATTCGATCCAGCACCTAGACAAGTCGAACCCGA  11 ThrProAspTyrPheLeu 306  11 ThrProAspTyrPheLeu 306  11 ACCCTGATTATTTTG 918  00 standard; DNA; 921 BP.	δ	261	_	lalleMetGlu	lleAspGl	
281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAs ::::::	81 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAs :::::	qa	781		CAATTCTTGAG	ATTGGAGA	
301	01 01	ò	8		rgGlnSerGlu	ProAspVa	
301 ThrProAspTyrPheLeu 30 	01 ThrProAspTyrPheLeu 30	Dp	841		GACAAGTCGAA	cccgarac	
901 ACCCCTGATTATTTTG 91	01 ACCCTGATTATTTTG 91 00 standard; DNA; 921 BP	ò	301	ThrProAspTyrPheLeu 30			
	00 standard; DNA; 921 B	qa	0	ACCCTGATTATTTTG 91			

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Hybridisation assay, genetic mapping, gene expression contraprotein identification; signal transduction pathway, metabo promoter, termination sequence, corn; ss.
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                                                                                                                                                                                                                          AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrj
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LysvalArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe:
                                                                 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl
                                                                                                                                                        LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGl
                                                                                                                                                                              AAGTATTTTACGGACCTTTTCGATTATCTCCCTCTTACAGCACTCATAGA
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                                                                                                                                                                                                                                                                           GATCGAATACAAGGTTCCACACGAAGGACCAATGTGCGATCTACTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                  Arabidopsis thaliana stress regulated gene SEQ ID NO 705.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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	Matches	529 AAAGTCCGTTACAGGATAGAATTACAATACTTCGAGGAAATCATGAGAGCAGCAAAATC 588 121 ThrGlnValTyrGlyPheTyrbsgluCysLeuargLysTyrGlyBanalaAsnValTrp 140 1589 ACTCAAGTGTACGGCTTCTATGATGAATGCTTAAGAAAATGGAAATGCAAATGTATGG 648	41 LysfyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 

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detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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- Web : www.genoscope.cns.fr)
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-MODEL=frame+ pAn.model -DEV=xlp
-MODEL=frame+ pAn.model -DEV=xlp
-MODEL=frame+ pAn.model -DEV=xlp
-CgnZ 1/USPTO spool p/USI0764259/runat_05122005_094548_7030/app_query.fasta_1.455
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LAODCL=0 -LAODFEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USRE-USI0764259 @CGN 1 1 8010 @runat_0512205_094548_7030 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBALOK=100 -LONGLOG
-DSP TIMEOUT=120 -WARN TIMEOUT=30 -THERADS=1 -XGAPCP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AY104802 Zea mays
BX8113410 Arabidops
BX814752 Arabidops
AY108657 Zea mays
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                - nucleic search, using frame_plus_p2n model
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CNSOADL7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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DB seq length: 200000000
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Direct Submission
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The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotat: V. Aury J.M., Jaillon O., Wincker P., Menard M., Cri Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the jennome released by MIPS (Munich Information center for Sequences). S prime and 3 prime are assembled with Plantp://www.genoscope.cns.fr/externe/sequences/Banque.
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HTC; GSLT CDNA.
Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core ei
rosida; eurosida II; Brassicales; Brassicaceae; Arab:

1 (bases I to 1285)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clep.

Menard, M., Craud, C., Quetter, F., Scarpelli, C., Schat

Temple, G., Caboche, M., Weissenbach, J. and Salanoubat

Whole Genome Sequence Comparisons and 'Full-Length'

A Combined Approach to Evaluate and Improve Arabidop:
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl
                                                                                                                          241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh
                                                                                                                                                                                                                                                              AsnTyrCysTyrArgCysGlyAsnMetAlaAla1leMetGluIleAspGl
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                                        GATGATCGATGGGGAATATCTCCACGAGGTGCTGGTTATACATT
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Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
UKGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_lengt,
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/clone="dSLTFB49ZD06"
/tissue_type="Rlowers and buds"
/ecotype="Col-0"
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/mol_type="mRNA"
/db_xref="texon:3702"
/clone="GSLTFB16ZA06"
/tissue_type="Flowers and bu
/cotype="Col-0"
/plasmid="pchVsPoRT 6"
complement(1. .1278)
/gene="At1g10430"
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HTC; GSLT CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (bases 1 to 1278)
Menard,M., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 ENTY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGY INRA : Clept C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) : S prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB16ZA06 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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                                          oAspAspArgCysGlyTrpGly1leSerProArgGlyAlaGlyTyrThrPheGlyGlnAs
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                    uAspArgIleGInGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPr
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US-10-764-259-13 (1-306) x CNSOADL7 (1-1250)	Oy 1 MetProSerTyralaAspValAspArgGlnIleGluGlnLeuSerGluCy:	Oy 21 SerGluLeuGluValLyBAsnLeuCy8AspGlnAlaArgThrIleLeuVa	Qy         41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGl:	61	81	Oy 101 LysValargTyrArgAspArg1leThr11eLeuArgGlyAsnHisGluSe:	Qy         121 ThrGlnValTyrGlyPheTyraspGluCysLeuArgLysTyrGlyAsnAli	Oy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeu1leGli 	161	Db 661 TTCTGTTTGCATGGAGGCCTTTCACCTTCTCTGGATACTCTTGACAATAT(   Qy	Oy 201 AspaspargCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPh.	Qy 221 IlealaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl;	Oy 241 ValMetGluGlyffyrAsnTrpCysGlnAspLysAsnValValThrValPhr 	Oy 261 ASHTYLCYSTYLAYGCYSG1yASHWELA1AAla1leMetG1u1leAspG1v 	Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa.:::::	Qy 301 ThrProAspTyrPheLeu 306 	RESULT 7 AY108657 LOCUS AY108657 LOCUS AY108657 DEFINITION Zea mays PC0069598 mRNA sequence. ACCESSION AY108657.1 GI:21211829 KEYWORDS HTC.
Db 957 AACTATTGCTACCGGTGTCGAAACATTGCTGCCATTCTAGAGATAAGAAGATACAAGAG 1016	Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300 s.:::::	301 ThrProAspTyrPheleu 306	Db 1077 ACCCTGATTGTGTCTTG 1094 RESULT 6 CNS0ADL7	Z	ACCESSION BX814752.1 GI:42474221 VERSION BX814752.1 GI:42474221 KEYWORDS HTC; GSLT cDNA. SOURCE Arabidopsis thaliana (thale cress)	-	<pre>REFERENCE 1 (Dates 1 to 1250)    AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,    Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,    Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.</pre>	TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation JOURNAL Unpublished	2 (bases 1 to 1250) Genoscope. Direct Submission	a a	full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.	URGY INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.	http://www.genoscope.cns.rr/externe/sequences/banque_brojet_br/full length http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. FEATURES Location/Qualifiers	source 1arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702"		gene complement(11250) /gene="At1g59830"	Alignment Scores: 6.67e-163 Length: 1250 Pred. No.: 1491.00 Matches: 270 Score: 1491.00 Conservative: 17 Best Local Similarity: 93.79\$ Mismatches: 19 Query Match: 89.28\$ Indels: 0 DB: 4 Gaps: 0

3B-2005

₹ 1020

3n 280

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SOURCE		e qq	372 GACCTCATCGAGCTCTTCCGCATCGGCGGCGACTCTCCCGACACCTA	.TG 431
		QQ dq	81 Glyasptyrvalaspargglytyrtyrservalgluthrvalserleule 	eu 100     G 491
AUTHORS		Oy 1	101 LysvalargTyrargaspargileThrileLeuargGlyasnHisGluse 	1e 120 
TITLE	Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization	Oy 1.	121 ThrGlnValTyrGlyPheTyrAspGluCySLeuArgLysTyrGlyAsnAl 	rp 140    GG 611
PUBMED PUBMED REFERENCE AUTHORS	Lanc Physiol. 134 (4), 1317-1326 (2004) 12020742 2 (bases 1 to 1534) Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,	Qy 1- Db 66	141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGl 	le 160 :: :TC 671
JOURNAL	ve np	Qy 1	161 PhecysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIl 	eu 180     TT 731
REFERENCE AUTHORS TITLE JOURNAL	3 (bases 1 to 1534) Coe, E.H. Direct Submission Submitted (25-878-2002) Maize Mapping Project, University of	Qy 1.	181 AspargiledinGluvalPro-HisGludlyProMetCysAspleuLeuT        :::	Pr 200    'CC 791
COMMENT	it you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,	Qy 2 Db 7	200 oASDASDArGCYSGlyTrpGly11eSerProArgGlyAlaGlyTyrThrF 	As 220    GA 851
0 0 0	<pre>www.riggr.org; or NUB1, www.nDD1.hlm.nln.gov. when the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.</pre>	Qy 2	220 pilealagluginpheasnHisThrashGlyLeuSerLeuValalaargA         :::	Le 240     CT 911
FEATURES	1. /mo_r	Qy 2, Db 9	240 uValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValE 	Pr 260     CC 971
	/db_xref="Malzeubk:e31/83" /db_xref="taxon:4577" /clone_lib="Malze Mapping Project/DuPont Cornsensus Library"	0y 20	260 oasnTyrcysTyrargCysGlyAsnMetalaalaileMetGluileAspC 	As 280 :: 3A 1031
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize	П	nArgSerPheLeuGlnPheGl ::::::           ccacaacrrccrrcaarrcaa	3L 300     CA 1091
ORIGIN	Mapping Project"	Oy 300	300 ysThrProAspTyrPheLeu 306 	
Alignment Scores Fred. No.: Score: Percent Similari Best Local Simil Query Match: DB:	Alignment Scores: 2.94e-161 Length: 1534  Pred. No.: 1478.00 Matches: 268  Score: 24 Conservative: 24  Best Local Similarity: 97.01\$ Mismatches: 14  Best Local Similarity: 87.01\$ Gaps: 0  DB: 4 Gaps: 0	SULT 8 SOADDH CUS FINITION	NSOADDH rabidopsis thaliana Fu LLPGH572E10 of Hormon rabidopsis thaliana (t	EB-2004
US-10-764-9 Oy Db	US-10-764-259-13 (1-306) x AY108657 (1-1534)         Oy       1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BX816593. BX816593.1 GI:42474290 HTC; GSLT_CDNA. Arabidopsis thaliana (thale cress) Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta;	phyta;
ò 8	21 SergluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluThrp 40	REFERENCE AUTHORS	Spermatophyta; magnollophyta; eualcotyledons; cole e rosids; eurosids II; Brassicales; Brassicaceae; Arat 1 (bases 1 to 1198) Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Cler	(anona
\$ 8 8	41 ASDVAlGINProvalLysCysProvalThrvalCysGlyAspIleHisGlyGlnPheHis 60	TITLE	Demara, M., Cruada, M., Weissenbach, J. and Salanoubat Temple, G., Caboche, M., Weissenbach, J. and Salanoubat Whole Genome Sequence Comparisons and 'Full-Length' A Combined Approach to Evaluate and Improve Arabidop	, uences: me
λo	61 AspLeulleGluLeuPheArg11eGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80 	JOURNAL	Annotation Unpublished 2 (bases 1 to 1198)	

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562   AAAAACTAATGAGCGTTTTCACTACCTTAGACAATCTCTTCTCTGTTTC   160	289 aProArgGlnSerGluProAspValThrArgLysThrProAspTyrPheLr
86868686868686	Db 10 RESULT 9 CRESULT 9 CRES189 LOCUS BEFINITION ACCESSION VERSION KEYWORDS SOURCE AUTHORS TITLE JOURNAL REPERENCE AUTHORS TITLE JOURNAL REPERENCE AUTHORS TITLE JOURNAL REPERENCE AUTHORS TITLE JOURNAL REPERENCE AUTHORS TITLE JOURNAL COMMENT COMMENT
Genoscope.  Direct Submission  Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 9100 GENEX cedex - FRANCE (B-mail : seqref@genoscope.cns.fr  - Web : www.genoscope.cns.fr)  The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V. Aury J.W. Jaillon O., Wincker P., Menard M., Cruaud C., URGV INRA : Clepet C., Cabbor, M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. Location/Qualifiers  ce /organism="Arabidopsis thaliana" /mol type="MRNA" /db Aref="Taxon:3702" /clone="GSLFPGH57ZF10" /clone="GSLFPGH57ZF10" /clone="GSLFPGH57ZF10" /plasmid="PorWySpORT" /gene="Atlg69960"	1.45e-155   Length:   1198
AUTHORS TITLE JOURNAL COMMENT COMMENT SOURCE GENE ORIGIN	Arighment Scores Scores:     Percent Similaria     Percent Similar

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UL-2004 ine) of

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Genoscope.

Joint Submission

Loud Submission

Submitted (20-JUL-2004) Genoscope - Centre National

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@ge-
Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) pri-
end enriched, double-strand cDNA was digested with N
into the Not I and EcoR V sites of the pCMVSPORT 6 v
was normalized. Library was constructed by Life Tech
division of Invitrogen.

Location/Qualifiers

/ord | 1.178
// -- | rune="MRNA"
                                                                             full-length cDNA clone CSODG004YK01 of B cells (Ramc Home sapiens (human).
                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Buarchontoglires; Primates; Cata Hominidae; Homo.

1 (bases 1 to 1758)

14, W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 GAGCTGGACCAGTGGATCGAGCAGCTGAACGAGTGCAAGCAGCTGTCCGA
                                                                                                                                                                                                                                                                              Contact : Feng Liang Email : fliang@lifetech.com URI
http://fulllength.invitrogen.com/ InVitroGen Corpore
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Homo sapiens (human)
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TITLE
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TITLE	Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome	ò	142 TyrPheThrAspLeuPheAspTyrLeuProLeu
JOURNAL	Annotation Unpublished 9 (honor 1 to 1021)	qq	see cacitcacigaicititigaitaicitccaciti
	. (bases 1 to 12/4) Genoscope. Direct Submission	λo	159
Ā	Submitted (18 NOV-2003) Genoscope - Centre National de Sequencage : BP 191 9106 BVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr	g :	626 AAAAACTAATGAGCGTTTTCACTACCTAGAC
COMMENT	equences are based Fechnologies (a di	දි සි	GACTTGACTACAGAACTCTTTTTTTTCTGTA
	ied out sequencing and O., Wincker P., Menard ach J., Salanoubat M.	\$ &	169 oSerLeuAspThrLeuAspHis1leArgAlaLet 
	OKAY INKA: Cleper.c., caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.	oy Oy	189 uGlyProMetCysAspLeuLeuTrpSerAspPro 
FEATURES	<pre>inc.pt.//www.genoscope.cmo.ii/cxceins/sequences/banque_riojec_br/ruii length http://www.genoscope.cms.fr/cgi-bin/ggb/ggb?source=Arabidopsis. location/Qualifiers</pre>	ò a	209 rProArgGlyAlaGlyTyrThrPheGlyGlnA6F 
	/organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="axon:3702"	δ g	229 nGlyLeuSerLeuValAlaArgAlaHisGlnLeu 
	/clone="GSLTPGHZZZA06" /tissue_type="Hormone Treated Callus" /ecotype="Col-0" /plasmid="pCMVSPORT 6"	රු පි	249 nAspLysAsnValValThrValPheSerAlaPro
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Oy Db	42 ValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAsp 61 		
3 Dp	62 LeuilegluLeuPheArgileGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGly 81 		
3 3	82 AspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLys 101 		
Oy 1 Db 4	102 ValargTyrargaspargileThrileLewargGlyasnHisGluSerargGlnIleThr 121 		
0y qû	122 GlnValTyrGlyPheTyraspGluCysLeuargLysTyrGlyAsnalaAsnValTrpLys 141 		

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qu	866 T	TCCTCGTGGTGCAGGCTACACTTTCGGACAAGATATCGCTACTCAGTTTA	4A 925
à	229 n(	nGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrA:	31 249
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QQ	986 A	: :	T 1045
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; Sequence 8, Application US/09928302
; Sequence 8, Application US/09928302
; Patent NO. 6818805
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: CATA E SILVA, OSWALDO DA
; APPLICANT: CHEN, ROUYING
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: PHOSPHARASE STRESS-RELATED PROTEINS AND N:
; TITLE OF INVENTION: PHOSPHARASE STRESS-RELATED PROTEINS AND N:
; TITLE OF INVENTION: 10 PLANTS
; FILE REFERENCE: 16313-0029
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; RIOR PAPLICATION NUMBER: 60/196,001
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PATENTIN VEY: 2.1
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-Q=/Cqm2 1/USPTO 2001 p/USIO764259/runat 05122005 094548 7041/app query.fasta_1.455
-Q=/Cqm2 1/USPTO spool p/USIO764259/runat 05122005 094548 7041/app query.fasta_1.455
-DB=168ued_Patents_NA -OFMT=fastap -SUFFIX=p2n.rni_-MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Sequence 543, Ap
Sequence 3, Appli
Sequence 596, Ap
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ITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets in the REFERENCE: P-PH 3457 USAGE TARGETS ACID TRUE REFERENCE: P-PH 3457 USAGE TARGET APPLICATION UNBER: US/09/300,958A URRENT APPLICATION NUMBER: US/09/301 USAGE TARGET APPLICATION NUMBER: 60/083,331 RIOR FILING DATE: 1998-08-27 RIOR APPLICATION NUMBER: 60/098,070 RIOR APPLICATION NUMBER: 60/118,624 RIOR FILING DATE: 1999-02-04 UWBER OF SEQ ID NOS: 85 US OFFWARE: Patentin Ver. 2.0 Q ID NO 39 USAGE TARGET APPLICATION UNBER: PATENT APPLICATION OFFWARE TARGET APPLICATION NUMBER: 60/118,624 RIOR FILING DATE: 1999-02-04 UWBER OF SEQ ID NOS: 85 USAGE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARGET APPLICATION OFFWARE TARG
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126   Pherytapolic/Steukrgivarycaltaliannalian	Alignment Scores: 6.17e-172 Length: 2182 Pred. No.: 6.17e-172 Length: 252 Score: 1427.00 Matches: 252 Percent Similarity: 94.35\$ Conservative: 32 Best Local Similarity: 83.72\$ Mismatches: 17
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US-10-764	-259-13 (1-306) x US-09-949-01	, APPLICANT: Jacquelin ; TITLE OF INVENTION:
δ	6	; TITLE OF INVENTION: ; FILE REFERENCE: RTS- ; CURRENT APPLICATION N
QQ Q	235 GAGCTGGÁCCAGTGGATCGÁGCAGCTGAACGAGTGCAAGCAGCTGTCCGAGTCCCAGGTC 294	CURRENT FILING DATE:
ò	26 LysasnLeuCysaspGlnAlaArgThrIleLeuValGluGluTrpasnValGlnProVal 45	; SEQ ID NO 3 ; LENGTH: 2966
g G		; TYPE: DNA ; ORGANISM: Homo sapie
승 음 상	46 LysCysProValThrValCysGlyAspileHisGlyGlnPheHisAspLeuIleGluLeu 65 :::	; FEATURE: ; NAME/KEY: CDS : LOCATION: (995)(1
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g q		Alignment Scores: Pred. No.:
ζ O	86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLygValArgTyrArg 105 	Score: Percent Similarity: Best Local Similarity: Query Match:
ò	106 AsparglleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGly 125	DB: 11S-10-764-259-13 (1-306)
qq	535 GAACGCATCACCATTCTTCGAGGGAATCATGAGGCGGACCAGATCACACAAGTTTATGGT 594	
8 8	PheTyraspQluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAsp	Cy 6 Aspvalaspa 
<b>Q</b> (	TICIAIGAIGAIGITTAAGAAAATAIGGAAATGCAAATGTTTGGAAATATTTTACAGAT	Qy 26 LysAsnLeuC
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ò	186 ValproHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspAspArgCysGly 205	Oy 66 PheArgiled
DP	775 GTTCCCCATGAGGGTCCAATGTGTGTTTTTTTTTTTTTT	6611
8 8	206 TrpGlylleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsplleAlaGluGlnPhe 225	Oy 86 ArgG1yTyrT               Db 1259 AGAGGATATT
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ò	266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln 285	146
qq		1439
ò	286 PheGlubroAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305	Oy 166 GlyLeuSerP
qα	1075 TITGACCCAGCACCTCGTAGAGGCGAGCCACATGTTACTCGTCGTACCCCCAGACTACTTC 1134	701
οχ	306 Leu 306	
Ор	1135 CTG 1137	Qy 206 TrpGlyileS
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ANTISENSE MODULATION OF PROTEIN PHOSPHAT;
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NUMBER: US/09/780,049
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: 96
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:CaGTGGATCGAGCAGTGAACGAGTGCAAGCAGCTGTCCGA
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TATTCAGTTGAAACAGTTACACTGCTTGTAGCTCTTAAGGT
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106 AsparglleThrileLeuargGlyAsnHisGluSerArgGlnIleThrGl:::	392	452 C 166 G 512 G	186	206 TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAl	226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMe	246 AENTEPCYBGINASPLYSASNVALTHEVALPHESERALAPFOASNTY	266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe	286 PheGlubroAlaProArgGlnSerGlubroAspValThrArgLysThrPr    :::	306 Leu 306	SULT 7
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	ng]n      3CAG	Qy         286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305           Db	Db 1919 CTG 1921 RESULT 6	US-949-U15-S444, Application US/09949016  ; Sequence 5464, Application US/09949016 ; GENERAL IN FORMATION:  GENERAL IN FORMATION:	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FIRE REFERENCE: CLOUISOT FIRE THE REFERENCE: CLOUISOT FIRE THE PROPERTY AND TOTAL TOWNED TO TO TO TO TO TO TO TO TO TO TO TO TO	CONCENT METALCHION NOMBER: 020/09/999,010  CURRENT FILING DATE: 2000-04-14  PRIOR APPLICATION NUMBER: 60/241,755  PRIOR FILING DATE: 2000-10-20  PRIOR FILING DATE: 2000-10-20  PRIOR PILING DATE: 2000-10-20	PRIOR FILING DATE: 2000-10-03  PRIOR PILING DATE: 2000-09-08  PRIOR FILING DATE: 2000-09-08  NIMBER OF ED. 11 NO.	NOTION OF SECULD NOS: 20.012  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 5464  LENGTH: 1522  TYPE: DAYS	; ORGANISM: Human US-09-949-016-5464	Alignment Scores:  Alignment Scores:  1411.00  Matches: 248  Scoret: 1411.00  Matches: 248  Percent Similarity: 93.69\$  Mismatches: 19  Mismat

3. 3.

Percent Similarity: Best Local Similarity Query Match: DB:	arity: milarity:	93.69% 82.39% 84.49% 3	Conservative: Mismatches: Indels: Gaps:	: 34 19 0		; Sequence 10, Apr ; Patent No. 64655; ; GENERAL INFORMAT; ; APPLICANT: Bre	0, Api 6465; FORMA: Bre
US-10-764-259	-13 (1-30	6) x US-09-94	9-016-590 (1-15	41)		; APPLICANT ; TITLE OF	INVENT
Oy 6 Db 46		ArgGlnIleGlu  :::  CAGTGGGTCGAG	nGlnLeuSerGluCysL            scagcrgaacgagrgra	AspValAspArgGln1leGluGlnLeuSerGluCysLysProLeuSerGluLeuGluVal::::::   :::   :::   :::    :::    :::	25	FILE REFER CURRENT A	RENCE PPLIC
7		ıCysAspGlnAla	ArgThrIleLeuValG		45	SEQ ID NO	SEQ.
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Oy 46		ovalThrvalCys	3GlyAspIleHisGlyG         :::        	LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu :::	65	; OKGANISM ; FEATURE: ; NAME/KEY	: Mus
•		eGlvGlvLvsAla	ProAspThrAsnTvrL	, 0	85	US-09-780-04	9-10
7				TTTAGAATTGGTGGAAAATCACGGATACAACTACTTATTCATGGGTGACTATGTAGAC	285	Alignment Scores Pred. No.:	ores:
		rTyrSerValGlu	ThrValSerLeuLeuV	ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg	10	Score: Percent Similarity Best Local Similar	larit; imila;
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Oy 126		gluCysLeuArg	JLYSTYrG1YASnAlaA	0.	14		6 Asp
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Qy 146		oTyrLeuProLeu	ThrAlaLeuIleGluH	LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly 	165	Oy 26	26 Lys/     80 AAG
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Sequence 10, Application US/09780049 Patent No. 6465250 GENERAL INFORMATION: APPLICANT: Brett P. Monia APPLICANT: Jacqueline Wyatt TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: 2001-02-09 CURRENT FILING DATE: 2001-02-09 INVENTION OF SEQ ID NOS: 96 SEQ ID NO 10 ILENGTH: 1781 TYPE: DNA ORGANISM: Mus musculus FEATURE: FEATURE: CORGANISM: Mus musculus FEATURE: CORGANISM: (196)(1125) US-09-780-049-10	4.98e-170 Length: 1781 1411.00 Matches: 250 y: 93.69\$ Conservative: 32 rity: 83.06\$ Mismatches: 19 84.49\$ Indels: 0	(1-306) x US-09-780-049-10 (1-1781)	AspValaspargGlnIleGluGlnLeuSerGluCysLysProLeuSerGluci:::::	LysasnLeuCysAspGlnalaArgThrIleLeuValGluGluTrpasnVa:     :::     ::::    :   AAGAGCCCTGCGAGAAGGCTAAAGAATCCTGACAAAAAAGAATCCAACGT	LysCysProValThrValCysGlyAsp1leHisGlyGlnPheHisAspLe:	TGTCCAGTCACTGTGTGTGGAGATGTACATGGCAATTTCATGATCT	Phakrg11eG1yG1yLysA1aProAspThrAshTyrLeuPheMecC1yAsh 	ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVa. 	AspargileThrileLeuargGlyasnHisGluSerargGlnIleThrGli :::	PheTyraspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTy: 	LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCy:	GlyLeuSerProSerLeuAspThrLeuAspHis11eArgAlaLeuAspAr;	CTGTCACCATCCATAGACACACTGGATCACATCCGAGCACTCGATCG	ValprohisgluglyprometCysaspLeuLeuTrpSerAspProAspAsj 	Trpdly11eSerProArgdlyAladlyTyrThrPheGlyGlnAsp11eAl:	GGGATATCTCCTCGGGGAGCTGGTTATACCTTTGGCCAAGATATTTC
Sequence 10, App Batent No. 64655 GENERAL INFORMAN APPLICANT: Bar APPLICANT: Bar APPLICANT: JAC TITLE OF INVENT TITLE OF INVENT TITLE OF INVENT FILE REFERENCE: CURRENT FILING NUMBER OF SEQ 10 SEQ ID NO 10 LENGTH: 1781 TYPE: DNA ORGANISM: WUS FEATURE: NAME/KEY: CDS LOCANISM: WUS FEATURE: LOCATION: (196	Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar. Query Match:	US-10-764-259-13	Qy 6 Asp' ::: Db 220 GAG	Oy 26 Lys.     Db 280 AAG	46	340	Oy 66 Phe.       Db 400 TTT	Qy 86 Argi 	Qy 106 Asp. ::: Db 520 GAG	Oy 126 Phe         Db 580 TTC		166	Db 700 GGT	Qy 186 Val     Db 760 GTT	206	Db 820 TGG

AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr 24	Qy         106 AspArg11eThr11eLeuArgG1yAsnHisG1USerArgG1n11eThrG1         1y 125           bb         634 GAGCGTATCACAATATTGCGAGGAAATCATGAAAGCCGGCAGATCACACA         3C 693	.25 593
880 AAICAIGGCCTCACGTIGGIGICCAGAGCTCACCAGCTGAGGGAGGATAT 93 246 ASnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 26 [	Qy         126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTy         .sp 14:           Db         694 TITTATGATGACCTACGAAAGTATGGGAACGCCAACGTGGGAAATA         AT 75:	145 753
266	Qy         146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCy         .ly 16:	165
286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe	Qy         166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspAr         -lu 18!	185
306 Leu 306 1110 ATC 1120	Qy         186 ValProdisGludlyProMetCysAspLeuLeuTrpSerAspProAspAs         1 y 205           Db         874 GTTCCACATGAGGCCCCAATGTGTGTGTCTTATGGTCAGATCCAGATGA         GC 933	205 933
RESULT 9	Qy 206 TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAl he 225	225 393
ייייי	Qy         226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMe         yr 245           Db         994 AACCATGCCAACAGGCCTCACAGGTGTCCCGTGCTCACCAGGTTGTAAT         3T 109	245 1053
TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT E TITLE OF INVENTION: EXPRESSION ; FILE REPERENCE: RTS-0130 CITEDERERNCE: RTS-0130 CITEDERER AND TAXATION NUMBER.	Oy 246 AsnTrpCygGlnAspLysAsnValThrValPheSeralabroAsnTy .rg 265	165 113
CURRENT FILING DATE: 2001-02-09; CURRENT FILING DATE: 2001-02-09; NUMBER OF SEQ ID NOS: 135; SEQ ID NO 10: 185; INDICATE: 1843; NUMBER OF SEQ ID NOS: 135; SEQ ID NO 10: 1843; NUMBER OF S	Qy 266 CysGlyasnMetAlaAlaileMetGluileAspGluThrMetAsnArgSe :In 285	285 1173
TYPE: DNA CREATURE Norvegicus FRATURE:	Qy         286 PheGluproAlaProArgGlnSerGluProAspValThrArgLysThrPr         'he 305           Db         1174 TTTGACCCAGCACCTCGTCGTGGAGCCTCATGTGACCCGGCGCACCCC         TC 123	. 233
; NAWE/ALT: CDS ; LOCATION: (310)(1239) US-09-780-045-10	Oy 306 Leu 306	
Alignment Scores:  Pred. No.: Score: Score: Pred. No.: 1411.00 Matches: Percent Similarity: Percent Similarity: 82.39\$ Mismatches: Query Match: 3 Gaps: 0	RESULT 10 US-09-780-045-3 ; Sequence 3, Application US/09780045 ; Patent No. 6602713 ; GENERAL INFORMATION:	
US-10-764-259-13 (1-306) x US-09-780-045-10 (1-1843)  Qy	; AFPLICANT: JACQUELINE WASTERNES ; TITLE OF INVENTION: ANTIGENES MODULATION OF PROTEIN PHOSPHATA ; TITLE OF INVENTION: EXPRESSION ; FILE REFRENCE: RTS-0130 ; CURRENT APPLICATION NUMBER: US/09/780,045 ; CURRENT PILING DATE: 2001-02-09	IC SUBUNIT BE
Qy 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValGlnProVal 45 :::       ::::   :::	; NOWBER OF SEQ ID NOS: 135 ; SEQ ID NO 3 ; LENGTH: 2574 ; TYPE: DNA	
Oy 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu 65 ::	; ORGANISM: Homo sapiens ; FRATURE; ; NAME/KEY: CDS ; LOCATION: (991)(1920)	
Oy 66 PheArgIleGlyGlyLyBAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp 85	lignment Scores: 8.96e-170 Length: 2	
Oy 86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg 105 	Percent Similarity: 93.69% Conservative: 34 Best Local Similarity: 82.39% Mismatches: 19 Query Match: 84.49% Indels: 0 DB:	

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                                                                                                      CGTTGCCCTGTTACTGTCTGTGGAGATGTGCATGGTCAATTTCATGATCTTATGGAACTC
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                                                                                                                                                                                                                                                                                     LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly
                  6 AspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGluLeuGluVal
                                                       26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValGlnProVal
US-10-764-259-13 (1-306) x US-09-780-045-3 (1-2574)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 11, Application US/09190976B
; Patent No. 6815107
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Stimulation of angiogenesis via syndecan-4 cytoplasmic domain signa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTAGAATTGGTGGCAAATCACCAGATACAAATTACTTGTTTATGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVa
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                                                                                                                                                                                  Mb storage
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb
COMPUTER: Dell PC
COMPUTER: Dell PC
COMPUTER: Microsoft Word version 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/190,976B
FILING DATE: 12-NO. 6815187-1998
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                        NAME: DAVIG PEASHKER, ESG.
REGISTRATION NUMBER: 29,633
REFERENCE/DOCKET NUMBER: BIS-041
TELECOWMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker,
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ 1D
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.71e-164
1366.00
92.36%
82.06%
81.80%
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Horowitz,
                                           SEOUENCES:
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Best Local Similarity:
                                          NUMBER OF
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± 6 7 2 7	292 CGACTATGTAAAATGGCGGTGGACGTTTGAGGAGGAGAATGTTAA  47 CysProValThrValCyGlyAsDIHSGLYGInPheHisAsDLeu11 he 66  15 CTGCTGTTACCATTTGTGGTGACGTACACGGTCAATTCCATGACTTGTT TC 411	ArglledlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTy       .rg         :::	472 GGATATTATICTGTTGAGACCGTATCTTACCTAGTTGCCATGAAAGTCAC  107 ArgileThrileLeuArgGlyAsnHisGluSerArgGlnileThrGlnVa he 126	TyraspGluCysLeuargLysTyrGlyasnalaasnValTrpLysTyrPh eu	147 PheAspTyrLeuProLeuThrAlaLeuIleGluHisGluHisGluHlePheCysLe   17 166   17 166   18 16   19 166   19 166   19 166   19 166   19 166   19 167   19 1	167 LeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIl	187 ProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspAr rp 206	207 GlylleserbroargGlyAlaGlyTyrThrPheGlyGlnAspllealaGl .sn 226 	227 HisThrasnGlyLeuSerLeuValalaargalaHisGlnLeuValMetGl .sn 246	247 TrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCy ys 266	267 GlyAsnMetAlaAlaileMetGluIleAspGluThrMetAsnArgSerPh 'he 286	287 GluProAlaProArgGlnSerGluProAspValThrArgLysThrProAs :::   ::	RESULT 13 US-09-614-221A-47 ; Sequence 47, Application US/09614221A ; Patent No. 6723837 ; GENERAL INFORMATION: ; APPLICANT: Karunanandaa, Balasulojini ; APPLICANT: Yu, Jaehyuk
Best Local S Query Match: DB: US-10-764-25 Qy Db 23	90 OV	oy oy	ያ ራ ይ	oy da	oy Q	ζζ Q	Qy	ος Op	çy Q	Qy	oy Oy	oy Q	RESULT US-09- ; Sequ. ; Patei ; APPI
Oy 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly 165	206 TrpGlylleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspileAlaGluGlnPhe 22 [1]	QY         226 ASINIASTINASHIS	Oy 266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln 285 	286 Phec	Oy 306 Leu 306 Db 1027 CFG 1029	RESULT 12 US-09-412-558B-269 ; Sequence 269, Application US/09487558B ; Patent No. 6949356 ; Patent No. 6949356	GENERAL INFORMATION: GENERAL TO STATE THE STAT	APPLICANT: MOLL Canally, Doug APPLICANT: Maxon, Mary APPLICANT: Milne, Todd	APPLICANT: Royer, John ; APPLICANT: Salama, Sofie ; APPLICANT: Sherman, Amir ; APPLICANT: Sherman, APPLICA	AFFLICANI: SILVA, OEIL AFFLICANI: Summers, Eric TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi FILE REFERENCE: 109272.130	CURRENT APPLICATION WOMBER: US/09/487,558B ; CURRENT FILING DATE: 0000-01-19 ; PRIOR APPLICATION NUMBER: US 60/487,558 ; PRIOR FILING DATE: 1999-10-20	) NOWHER OF SEQ ID NOS: 446 ; SEQ ID NO 269 ; LENGTH: 1134	; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-09-487-558B-269 Alignment Scores: 5.53e-155 Length: 1134 Pred. No.: 5.53e-155 Matches: 229 Score: 1291.00 Matches: 229 Percent Similarity: 87.67% Conservative: 34

; APPLICANT: Kishore, Ganesh M. ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED ; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM ; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM		k o	247 TrpCysGlnA     928 TGGTCTCACO
; FILE REFERENCE: 10016017; CURRENT APPLICATION NUMBER: US/09/614,221A; CURRENT FILING DATE: 2000-07-12; PRIOR APPLICATION NUMBER: US 60/142,981		ò 8	267 GlyasnMet/        988 GGTAATCAA(
; PRIOR FILING DATE: 1999-07-12; NUMBER OF SEQ ID NOS: 626		ò	287 GluproAlai
; SEQ ID NO 4'; ; LENGTH: 1110 ; TYPE: DNA		Db 1(	1048 GACCCATCC
) OKGANISM: Saccharomyces cerevisiae US-09-614-221A-47		RESULT 14 US-09-487-558B-267	558B-267
Alignment Scores: 2.33e-154 Length: 1110  Pred. No.: 1286.00 Matches: 27  Percent Similarity: 87.33 Conservative: 35  Best Local Similarity: 75.67 Mismatches: 38  Ouery Match: 37.01 Indels: 0  DB: 3000000000000000000000000000000000000		) Patent Co ; ) Patent IN ) GENERAL IN APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT	Sequence Act, Applicate Patent No. 6949356 GENERAL INFORMATION: APPLICANT: Busby, Rol APPLICANT: Cali, Br: APPLICANT: Hecht, Pe APPLICANT: Holtzman APPLICANT: Madden, P
US-10-764-259-13 (1-306) x US-09-614-221A-47 (1-1110)		, APPLICANT , APPLICANT	
Qy 7 ValAspArgGlnIleGluGlnGlnCeuSerGluCysLysProLeuSerGluLeuGluValLys 26 :::	7	; APPLICANT; APPLICANT; APPLICANT; APPLICANT	
Qy 27 AsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValGlnProValLys 46		; APPLICANT; APPLICANT; TITLE OF	APPLICANT: Silva, Of APPLICANT: Summers, TITLE OF INVENTION: P
47 CysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeuPhe		CURRENT CURRENT	CURRENT APPLICATION I CURRENT FILING DATE: PRIOR APPLICATION NU
328 GIGCCIGITACCAITIGIGGIGACGIACACGICAAITCCAIGACITGITAGAACTITIT	7	PRIOR F.	PRIOR FILING DATE: 1 NUMBER OF SEQ ID NOS
Oy 67 ArgileGlyGlyLysAlabroAspThrAsnTyrLeuPheMetGlyAspTyrValAspArg 86 :::		; SOFTWARE: Pate ; SEQ ID NO 267 ; LENGTH: 1110	3: Patentin v. 0 267 : 1110
Oy 87 GlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArgAsp 106	9	; ITE: DNA ; ORGANISM: US-09-487-558	DNA SM: Saccharom 558B-267
107 ArgileThrileLeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGlyPhe		Alignment Scores Pred. No.: Score:	Scores:
SOB AGANTIACCATACTCAGAGGCCAATCACGAGTCTAGGCAGATTACCCAAGTATACGGGGTTTTTTTT	, 9	Percent Sim Best Local ( Query Match DB:	Percent Similarity: Best Local Similarity: Query Match: DB:
568 TATGATGAATGTTTGAGAAAGTACGGCAGTGCAAACGTGGGAAATGTTCACAGATCTT	7	US-10-764-	US-10-764-259-13 (1-306
UY 14/ Prockaptyreurzoceurrzataeurieciumiserulieciumiserulieciatyriy 166  Db 628 TTCGATTATTTCCTATAACCGCATTAGTAGATAATAAAATTTTCTGTCTG	2 6		7 ValAspArg(
Oy 167 LeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGluVal 186	9	 8 8	208 CTTGACCAA
688 CTTTCCCCCATGATAGAAACCATAGATCAGGTGAGAGAGTTGAACAGAATACAGGAAGTG	7		 268 CGACTATGE
Qy         187 ProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGlyTrp         206	- 4		47 CysProval
Cy 207 GlylleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPheAsn 226	9		328 GTGCCTGTT
808 GGAATCAGTCCCAGAGGTGCAGGCTTCACTTTTGGACAGAGTGTCAGTGAGCAATTCAAT	7	6 G	67 ArgileGly :::       388 AAGATTGGT
Oy 227 HisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsn 246	9	c o	87 GlyTyrTyr:          448 GGATATTAT

TrpCysGlnAspLysAsnValValThrValPheSerAlaBroAsnTyrCy: 	rCy: /s 266 
GIYABNMETALAALAILEMETGIUILEASDGIUTHKMETASNAKGSEKPh 	rPh: 18 286    :: 18 ATT: 1C 1047
GlubroAlabroArgGlnSerGlubroAspValThrArgLysThrProAsj :::    ::	oAs) 3u 306                     AGA' "A 1107
ESULT 14 S. 09-487-558B-267 Bequence 267, Application US/09487558B Patent No. 6949356 GENERAL INFORMATION: APPLICANT: Busby, Robert APPLICANT: Busby, Robert APPLICANT: Hecht, Peter APPLICANT: Madden, Kevin APPLICANT: Madden, Kevin APPLICANT: Madden, Kevin APPLICANT: Madden, Kevin APPLICANT: Madden, Kevin APPLICANT: Madden, Kevin APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman, Amir APPLICANT: Soleman, Amir APPLICANT: Soleman, Amir APPLICANT: Soleman, Amir APPLICANT: Soleman, Amir APPLICANT: Soleman, Amir APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman, Sofie APPLICANT: Soleman,	lite :ion in Pungi
Alignment Scores:  2.33e-154 Length: 1110 Score: Score: 1286.00 Matches: 227 Percent Similarity: 87.33 Conservative: 35 Best Local Similarity: 75.67% Mismatches: 38 Query Match: 77.01% Indels: 0 DB:	
US-10-764-259-13 (1-306) x US-09-487-558B-267 (1-1110)	
ValaspargdinilediudinieuserdiucysiysProleuserdiulei:::    :::	ule: 78 26 
AsnleucysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValGlı 	G 1 /8 46  ::  TAA: 1C 327
CysprovalThrvalCysGlyAspIleHisGlyGlnPheHisAspLeuIl+ 	uIl: 1e 66  ::    GTT; IT 387
ArgileGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTy: :::	pTy: cg 86         3h 447 TTA( 3A 447
GlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValAr<	Arr

ch completed: December 9, 200 time : 212 secs	Search Job tim	Pred. No.: 3.19e-135 Length: 1339 Score: 1137.50 Matches: 204 Percent Similarity: 81.43\$ Conservative: 46 Best Local Similarity: 66.45\$ Mismatches: 56 Query Match: 68.11\$ Indels: 1 DB: 3 Gaps: 1
1004 cccgracccaacracrrccr	qq	
301ThrProAspTyrPheLe	ò	; ORGANISM: Human US-09-949-016-2909
944 AAAGATTTCATCATCTTTGA	qa	; LENGTH: 1339
281 ArgSerPheLeuGlnPheGl	ò	T S
884 AACTACTGCTACCGCTGTGG	q	; PRIOR APPLICATION NUMBER: 60/231,498 ; PRIOR FILING DATE: 2000-09-08 . NIMBER OF SEC IT NOS. 202019
261 AsnTyrCysTyrArgCysGl	ζō	; PRIOR APPLICATION NUMBER: 00/23/, /08 ; PRIOR FILING DATE: 2000-10-03 ; TILING TO THE TOWN
824 GTGATGGAAGGTTACAAGTG	q	; PRIOR APPLICATION NUMBER: 60/241,755 ; PRIOR FILING DATE: 5000-10-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-
241 ValMetGluGlyTyrAsnTr	ð	; CURRENT APPLICATION NUMBER: US/09/949,016 ; CURRENT FILING DATE: 2000-04-14
	<b>3</b> 원	; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CL001307
704 GAAGACACCACAGGCTGGGG	셤 ;	; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. . THITE OF INTERMEDIAL DAY VANDENITAME IN VANDENI ACCURATED
201 AspAspArgCysGlyTrpGl	γ	. Sequence 2909, Application US/09949016 ; Patent No. 6812339
644 GACCGAAAGCAAGAGGTGCC	QQ	RESULT 15
584 TTCTGCGTGCACGGGGGCCT	g &	Oy 287 GlubroAlaBroArgGlnSerGluBroAspValThrArgLv8ThrBroAspTyrBheLeu 306 
161 PheCysLeuHisGlyGlyLe	λ	Db 988 GGTAATCAAGCTATCATGGAAGTGGACGAGAATCATAATAGACAATTCTTACAGTAC 1047
	q	Oy 267 GlyAsnMetAlaAla1leMetGluIleAspGluThrMetAsnArgSerPheLeuGlnPhe 286
141 LysTyrPheThrAspLeuPh	ò	Db 928 TGGTCTCACCAGCAAAATGTTGTCACCATTTTCAGTGCTCCTAATTACTGCTACAGATGT 987
	; A	247 TrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArgCys
404 AAGGTTCGCTATCCTGATCG	음 &	Oy 227 HisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsn 246
	ò	808 GGAATCAGTCCCAGAGGTGCAGGCTTCACTTTTGGACAAGATGTCGGTGAGCAATTCAAT
344 GGGGACTTTGTGGACCGTGG	qq	Qy         207 Gly1leSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp1leAlaGluGlnPheAsn         226
81 GlyAspTyrValAspArgGl	λ	Db 748 CCTCATGAAGGTCCTATGTGTGCTCTTATGGTCAGACCCTGACGATAGAGGGCGGATGG 807
	qa	
224 AACGTGCAGAGGGTGGACTC	윰 &	Oy 167 LeuserProSerLeudsphriedhenghislledhadhalleudsphrgjledhadul 186
41 AsnValGlnProValLysCy	λŏ	628 TTCGATT
	q	Oy 147 PheAspTyrLeuProLeuThrAlaLeuIleGluHisGluHlePheCysLeuHisGlyGly 166
21 SerGluLeuGluValLysAs	ò	Db 568 TATGATGATGTTTGAGAAAGTACGGCAGTGCAAACGTGGAAAATGTTCACAGATCTT 627
I MetProserTyrAlaABDVA      :::   :: 104 ATGGCGAGATCAGCGACCT	<b>₹</b> 6	Oy 127 TyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAspLeu 146
.0-764-259-13 (1-306) x US-09-9	:	107 ArgileThrileLeuArgGlyAsnHisGluSerArgGlnileThrGlnValTyrGlyPhe

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rp 140
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|GG 523
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:TC 583
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.TC 163
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AT 283
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TG 343
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|TT 403
                                                                                                       le 120
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TC 463
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                                   GC 223
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              AshleucysAspGlnAlaArgThrIleLeuVa
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GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: WAN THIELEN, NOCHA
APPLICANT: GINTENTION: PROSPHYTASE
TITLE OF INVENTION: PROSPHYTASE STRESS-RELATED PROTEINS AND M
TITLE OF INVENTION: PROSPHYTASE STRESS-RELATED PROTEINS AND M
TITLE OF INVENTION: IN PLANTS
FILE REFERENCE: 16313-0029
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 8
    US-10-437-963-40723

US-09-938-842A-705

US-09-938-842A-571

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US-10-425-115-149113

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Matches:
Conservative:
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Indels:
Gaps:
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Patent No. US20020152502A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-302-8
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-Q=/cgn2 1/USPTO_spool p/US10764259/runat 05122005 094549 7075/app_query.fasta_1.455
-Q=/cgn2 1/USPTO_spool p/US10764259/runat 05122005 094549 7075/app_query.fasta_1.455
-DB=Published Applications NA Main - QFWT=fastap - SUFFIX=p2n.rnpbm
-MINMATCH=0.1_-LOOPCL=0 - LŌOPEXT=0 - UNITS=bits - START=1 - END=-1
-MATRIX=blosume.2 - TRANS-humanat0.cdi - L1ST=45 - DOCALIGN=200 - TRR SCORE=pct
-TRR MAX=100 - TRR MIN=0 - ALIGN=15 - MODE=LCCAL - OUTFWT=pto - NORM=ext
-USRE-US10764259 @CGN 1 1.1549 @tunnat 05122005 094549 7075 - NCFU=6 - ICPU=3
-NO WMAP - LARGEQUERY - NEG_SCORES=0 - WĀIT - DSPBLOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DBLEXT=7
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2: /cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
5: /cgn2 6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-764-259-8
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                                                                                41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis
                                                                                           AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet
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              Met ProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu
                                                 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp
US-10-764-259-13 (1-306) x US-09-828-302-8 (1-1365)
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Publication No. US20040148658A1
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
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       APPLICANT: CHEN, ROUYING
APPLICANT: ISHITANI, MANABU
TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND MI
TITLE OF INVENTION: PROSPHATASE
TITLE REFERENCE: 16313-0029
CURRENT FALLICATION NUMBER: US/10/764,259
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 46
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CRGANISM: Physcomitrella patens
US-10-764-259-8
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VAN THIELEN, NOCHA
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221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl

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Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAsplysAsnValValThrValPheSerAlaPro 260	–υ н	TT 451
Oy 261 ASnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGlu1leAspGluThrMetAsn 280		  GG 511
281 ArgserPheieuGlnPheGluProAlaProArgGluBroArgValThrArglys	512 AAATACTTTACAGACTTGTTTGATTATTTGCCTCTGACTGCTCATTGA	
Db 911 CGGTCTTTTCTTCGAACCAGCACCGGGCAAGTGAACCAGATGTGACGGGAAG 970 Ov 301 ThrProbentvrDbelan 306	Oy 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisI]	eu 180
Db 971 ACTCCTGATTACTTTCTG 988	181 AspargileGinGluValProHisGluGlyProMetCysAspLeuLeuTr	
REGULT 3 US-10-236-699-21	Db 632 GATCGTATTCAAGAGGTTCCACATGAAGGACCAATGTGTGTCTTGTC C	CT 691
; Sequence 21, Application US/10236699 ; Publication No. US20030150028A1 ; GENERAL INFORMATION:	Qy         201 AsphaphrgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPh         .s           Db         692 GATGATCGCTGTGGATGGGGAATATCTCCACGTGGTGCAGGATACACATT         .a	.sp 220     AT 751
; APPLICANT: BOHNERY, HANS J. ; APPLICANT: CHEN, RUOYING ; APPLICANT: ISHITANI, MANABU ; APPLICANT: VAN THIELEN, NOCHA	Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl e	eu 240    TT 811
; AFFLICANI: COSIA E SILVA, CSMALLO DA ; TITLE OF INVENTION: PROFIEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND ; TITLE OF INVENTION: METHODS OF USE IN PLANTS ; FILE REFERENCE: 16313-0161	Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh	ro 260     CA 871
; CURRENT APPLICATION NUMBER: US/10/236,699 ; CURRENT FILING DATE: 2002-09-05 ; PRIOR APPLICATION NUMBER: 60/317,305 ; PRIOR FILING DATE: 2001-09-05	Qy         261 AsnTyrCysTyrArgCysGlyAsnMetAlaalaIleMetGlulleAspGl         :	sn 280 :: AT 931
; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 21 ; LENCTH: 1386	Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVə :::::	ys 300     -  - AG 991
; ORGANISM: Glycine max US-10-236-699-21	Qy 301 ThrProAppTyrPheLeu 306 	
Alignment Scores: Pred. No.: Score: Score: Score: Fercent Similarity: Percent Similari	RESULT 4 US-10-236-699-31 ; Sequence 31, Application US/10236699 ; Publication No. US20030150028A1 ; GENERAL INPORMATION: . APPLICANT: HOHNERT, HANS J	
10-764-25	; APPLICANT: CHEN, RUOYING ; APPLICANT: ISHITANI, MANABU ; APPLICANT: VAN THIELEN, NOCHA ; APPLICANT: COGTA E SILVA, OSWALDO DA	
::	SSS-RELATED POLYPE	Ď.
Qy     21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40	; TIDE REFERENCE: 10312-0101 ; CURRENT FILING DATE: 2002-09-05 ; PRIOR APPLICATION NUMBER: 60/317,305	
Qy       41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60         L	; PRIOR FILING DATE: 2001-09-05 ; SUFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 31	
Qy 61 AspLeulleGluLeuPheArgileGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80	; LENTH: 1330 ; TYPE: DNA ; ORGANISM: Oryza sativa US-10-236-699-31	
Oy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100 	Alignment Scores: 1.95e-199 Length: 1330 Pred. No.: 1547.00 Matches: 280	

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Percent Sim Best Local Query Match DB:	Percent Similarity: 96.41% Conservative: 15 Best Local Similarity: 91.50% Mismatches: 11 Query Match: 92.63% Indels: 0 DB: 6	7.6.
US-10-764-	-259-13 (1-306) x US-10-236-699-31 (1-1330)	, APPLICANT: CI , APPLICANT: II
δ	1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20	; APPLICANT: ; APPLICANT: ; TITLE OF INV
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k d	21 SerGluLeuGluValLysAsnLeuCysBaspGlnAlaArgThrIleLeuValGluGluTrp 40	CURRENT APPLIA CURRENT FILING PRIOR APPLICA
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6 G	224 AACGIGCAACCGGTGAAGTGCCCCGTCACCGTCTGCGGCGATATTCACGGCCAGTTTAC 283	SOFTWARE: Pate ; SEQ ID NO 7
ò	61 AspleulleGluLeuPheArgileGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80	; LENGTH: 1243 ; TYPE: DNA
qq	284 GATCTCATCGAGCTGTTTCGGATTGGAGGGAACGCACCCGAIACCAATTATCTCTTCAIG 343	, ORGANISM: Bra US-10-236-699-7
ò	81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100	Alignment Scores Pred. No.:
qo	344 GGTGATTATGTAGATCGTGGATACTATTCAGTGGAGACTGTTACACTTTTGGTGGTGGTTTTG 403	Score: Percent Similar
ර ස	LysValArgTyrArgAspArg1leThr1leLeuArgGlyAsnHisGluSerArgGlnIle	Best Local Simila Query Match:
an i	AAAGICCGTTACAGAGATAGAATCACAATTCTCAGGGAAATCATGAAAGTCGTCAAATT	
È	ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp	US-10-764-259-13
qq	464 ACTCAAGTGTATGGCTTCTATGATGATGCTTGAGAAATATGGAAATGCCAATGTCTGG 523	Oy 1 Me
<i>δ</i>	141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluHie 160	Db 150 ÅT
ପ୍ଧ	524 AAATACTTTACAGACTTGTTTGATTATTTACCTCTGACTGCCCTCATTGAGAGTCAGATT 583	Qy 21 Se
'n	161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180	Db 210 1C
Dp	584 TICTGCTTGCATGGAGGTCTCTCTCTCTTTGGATACATGGGATACATCAGAGCATTG 643	Qy 41 As:
ò	181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200	Db 270 AA
qq	644 GATCGTATACAAGAGGTTCCACATGAAGGACCAATGTGGATCTCTTGTGTGTG	Qy 61 As;
ò	201 AspaspargCysGlyTrpGlyIleSerProArgGlyAlaGlyTrThrPheGlyGlnAsp 220	Db 330 GA
Db	704 GATGATGGCTGGGGGAATATCTCCACGTGGTGCAGGATACACATTTGGACAGGAT 763	Qy 81 G1
δ	221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240	DP 390 GG
QQ	764 ATAGCTGCTCAGTTTAATCATACCAATGGTCTCTCCCTGATATCGAGAGCTCATCAGCTT 823	Qy 101 Ly
λ̈́O	241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260	Db 450 AA
Dρ	824 GTTATGGAAGGATTCAATTGGTGCCAGGACAAAATGTGGTGACTGTATTTAGTGCACCA 883	Qy 121 T
Š	261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlalleMetGluIleAspGluThrWetAsn 280	Db 510 AC
Op Q	884 AATTACTGTTACCGATGTGGGGAATATGGCTGTATACTAGAAATAGGAGAGAATATGGAT 943	Oy 141 Ly
δ,	281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300	Db 570 AA
οp	944 CAGAATTTCCTTCAGTTTGATCCAGCGCCCAGGAAATTGAGCCTGACACACAC	Qy 161 Ph
ò	301 ThrProAspTyrPheleu 306	TT 630 TT
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                             : CHEMAN, MANABU
: ISHITANI, MANABU
: COSTA E SILVA, OSWALDO DA
INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPE)
INVENTION: METHODS OF USE IN PLANTS
RENCE: 16313-0161
RENCE: 16313-0161
RELING DATE: 2002-09-05
ILLING DATE: 2001-09-05
ING DATE: 2001-09-05
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APPLICANT: La ROVALIC, David K.

APPLICANT: Zhou, Yihua
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APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad
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Mismatches:
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_44137C.1
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Matches:
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               , OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE90H04_FLI
US-10-425-114-35277
                                                                                                                                                                                                                     US-10-764-259-13 (1-306) x US-10-425-114-35277 (1-1732)
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:::          :::      :::      :::	Oy 60 HisAspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAs::	Oy 80 MetGlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLe	Qy 100 LeulysValargTyrargAspargllethr11eLeuargGlyAsnHisGl 	Qy 120 IleThrGlnValTyrGlyPheTyrAspGluCysLeuArglysTyrGlyAe 	Qy 140 TrpLysTyrPheThraspLeuPheAspTyrLeuProLeuThralaLeuIl 	Qy 160 IlePheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHi :::	Qy 180 LeuAspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLe 	Qy 200 ProAspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrTh 	Oy 220 AspilealadludinPheAsnHisThrAsnGlyLeuSerLeuValAlaAr           :::	Qy 240 LeuValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrVa 	Qy 260 ProAsnTyrCysTyrArgCysGlyAsnMeralaAlaIleMetGlulleAs	Qy 280 AsnArgSerPheLeuGlnPheGluBroAlaBroArgGlnSerGluBroAs ::::::::	Qy 300 LysThrProAspTyrPheLeu 306 	RESULT 10 US-09-938-842A-705 ; Sequence 705, Application US/09938842A ; Patent No. US20020160378A1 ; GENERAL INFORMATION: ; APPLICANT: Harper, Jeff ; APPLICANT: APPLICANT: Mang Yune	APPLICANT: Zhu, Tong TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGE TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-5 CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24
Qy       160 11ePheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAla       179         bb       481 GTGTTCTGCCTTCAGGGTGGTCTCTCCATCATTGGATACTTTAGATAACATCCGTGCT       540         Qy       180 LeuAspArgIleGInGluValProHisGlyGlyCyproMetCygAspLeuLeuTrpSerAsp       199	ACAGAGGTTCCTCATGAAGGACCCATGTGTGTTTTTTTTT	Db 601 CCAGATGACAGATGCGGGTGCGGAATTTCACCGAGAGGAGCAGGTATATGGCCAA 660  Qy 220 AspileAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGln 239	-⊢ >-	Db 721 CTIGTANIGGAGGATTAATHGFTCAGGACAAGATGTTGTGAGGTCTTCAGGTG 780  Qy 260 ProAshTyrCysTyrArgAshMetAlaAlalleMetGlulleAspGluThrMet 279	Db 781 CCAAACTACTTATCGCTGTGGTGTGTTTTTTGAATTGGCGAATTGGTGAAAACATG 840  280 AsnArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrarg 299	Db 841 GATCAGAACTTCTCCAATTTGATCCAGCAAATTGAACCAGACACACGC 900  Qy 300 LysThrProAspTyrPhelieu 306	Db 901 AAGACTCCCGACTACTTTTG 921	S-10-236-699-25 Sequence 25, Application Publication No. US2003015 SEGUERAL INFORMATION:	APPLICANT: CHEN, RUOYING APPLICANT: ISHITANI, MANABU APPLICANT: VAN THIELEN, NOCHA		CURRENT FILING DATE: 2002-09-05; CURRENT FILING DATE: 2001-09-05; PRIOR APPLICATION NUMBER: 60/317,305; PRIOR FILING DATE: 2011-09-05; PRIOR FILING DATE: 2011-09-05	ഗ		Alignment Scores:  Alignment Scores: Score: Score: Score: 1508.50 Matches: 272 Percent Similarity: Best Local Similarity: 90.33	ProSerTyrAlaAspValAspArg 

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US-09-38-842A-705
US-09-38-842A-705
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Sequence 705, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
FAPPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Tan, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGEI
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND WETHODS OF USE
FILE REPERENCE: SCRIPIJOG-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 705
LENGTH: 921
TYPE: DNA
CREANISM: Arabidopsis thaliana
US-09-938-842A-705
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Publication No. US20040009476A9; GENERAL INFORMATION: APPLICANT: Harper, Jeff APPLICANT: Herps, Joe1 APPLICANT: Herps, Joe1 APPLICANT: Wang, Xun APPLICANT: Wang, Xun TITLE OF INVENTION: SAME, AND METHODS OF USE TITLE OF INVENTION: SAME, AND METHODS OF USE TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3; CURRENT APPLICATION NUMBER: US 60/227,866 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-6-22 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 571 LENGTH: 924 TYPE: DNA ORGANISM: Arabidopsis thaliana US-09-938-842A-571	Alignment Scores:  Alignment Scores:  Proced. No.:  1.34e-192  Matches:  Score:  1495.00  Matches:  268  Percent Similarity:  95 41\$  Conservative: 23  Best Local Similarity:  95 52\$  Mismatches: 14  Conservative: 23  Best Local Similarity:  95 52\$  Conservative: 23  Mismatches: 14  Indels: 0  Gaps: 0  Conservative: 23  Best Local Similarity: 89.52\$  Gaps: 0  Conservative: 23  Best Local Similarity: 89.52\$  Conservative: 23  Best Local Similarity: 89.52\$  Gaps: 0  Conservative: 23  Gaps: 0  Conservative: 23  Gaps: 0  Conservative: 23  Gaps: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Conservative: 24  Indels: 0  Indels: 0  Conservative: 24  Indels: 0	Db 187 CTAATCAACCATTTTCCTATACTTCTCCTCATACTAATTACTTTTCATGGGT 246  Oy 82 AspTytValAspArgGlyTytTySerValGluThrValSerLeuLeuValAlaLeuLys 101  247 GATTATGTTGATCGAGGGTATTATTCTGTGAGACACTCTCACTTTTCGTAGCACTGAAA 306  Oy 102 ValArgTyAragAspArg11eThr11eLeuArgGlyAsnHisGluSerArgGln1leThr 121  Sof GTTCGTTACAGAGATTACTACTACCTAGAGACACTCTCACTATACT 366  Oy 122 GlnValTyTaCATAGATTACTACTACTACTAGAGAGATACTTGAAATTACT 366  Oy 124 GATTATACATAGAGATTACTACTACTAGAGAGAATACTGAAACTACTAGAATTACT 366  Oy 125 GlnValTyTaCATGATGATGATGATGATGTATGAATTACT 366  Oy 142 TyrPheThrAspLeuPheAspTyTLeuProLeuThrAlaLeu1leGluHisGluIlePhe 161  142 TyrPheThrAspLeuPheAspTyTLeuProCactTACAGAATTACTAGAGATCAGAATTACT 486  Oy 162 CysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIlleArgAlaLeuAsp 181  Oy 162 CysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIlleArgAlaLeuAsp 181  Oy 163 TGTTTACATGAGAGACTTTCACCTTATAGAGAACTCCGATCTTAGAT 546  Oy 164 TGTTTACATGAGAGACTTTCACCTTTATAGATACCTTGACACACCTCAGATCAGAT 606  Oy 165 CysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIlleHill

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	US-10-425-115-160546 Alignment Scores:
1167	) ORGANISM: Zea mays ; FRATURE:
Oy 196 uTrpSerAspProAsp	TYPE: DNA
Db 1107 TGTCCGCTCCCTTGAT	; NUMBER OF SEC ID NOS: 369326 ; SEO ID NO 160546
Oy 176 sIleArgAlaLeuAsp	; Fild Kerkenens: 38-21(33221)8 ; CURRENT APPLICATION VONDER: US/10/425,115 ; CURRENT FILING DATE: 2003-04-28
1047	; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION: Plants ; PITLE DEPENDENCE. 30-21(2)2318
, T	; APPLICANT: Zhou, Yihua ; APPLICANT: Cao, Yongwai
Oy 136 nAlaAsnValTrpLys	; GENERAL INFORMATION: ; APPLICANT: La Rosa, Thomas J. ; APPLICANT: La Rovalic, David K.
	; Sequence 160546, Application US/10425115 ; Publication No. US20040214272A1
Qy 124	RESULT 15 US-10-425-115-160546
Db 867 TCACTTGGTCTGGTTT	Db 1092 AAACCCCAGACTTTTTG 1111
Qy 123	Oy 300 ysThrProAspTyrPheLeu 306
Db 807 ACTGTAGATTCAGATG	
	280 nAT
Oy 123	NTYICYSTYIAIGOSSIYASIMAtAlaAlaIleMetGluIleAspGluThimetAs
Db 687 ACTCAAGTGTATGGCT	Db 912 IGTAATGGAAGGATTAATTGGTGCCAGGATAAGAATGTAGTCACAGTCTTCAGTGCGCC 971
Qy 121 ThrGlnVal	Qy 240 uValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPr 260
OY 101 LYSVALAFGIYFAFGA 	Db 852 CATTGCGCAGCAGTTCAACAAACGGTCTTTCTCTCATTTCAAGGCCCATCAACT 911
Db 567 GGCGACTACGTCGACC	792 AGATGACCGATGTGGATGGGGAATTTCACCAAGAGGAGCAGGTTACACATTTGGGCAAGA
Qy 81 GlyAspTyrValAspA	200 oAs
Db 507 GACCTCATCGAGCTCT	Db 732 GATCGCGTACAGGAGGTTCCTCCCATGAAGGACCCATGTGTGTG
Qy 61 AspleulleGlubeuP	Oy 181 AspArglleGlnGluValPro-HisGluGlyProMetCysAspLeuLeuTrpSerAspPr 200
Oy 41 AsnValGlnProValL               Db 447 AACGTGCAGCCCGTGC	OY 161 PACCYSLEWINSGLY3/YEUSSCFICOSETLEWISPITHICAPHISITEATGALEW 180
Db 387 CCTGAGGCGGAGGTCA	Db 612 AAGIAITTTACAGACTIGITTGATTTTTGCCTCTCACAGCTCTTATAGAAAATCAGGTC 671
Db 327 AIGCCAICGCACGCGC	552 ACT
Qy 1 MetProSerTyrAlaA	Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
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Length:
Matches:
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Search completed: December 9, 2005, 13:12:22 Job time : 833 secs

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APPLICANT: Beau, Christine
APPLICANT: Bennett, C. Frank
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APPLICANT: Griffey, Richard H.
APPLICANT: Barker, Brenda F.
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Publication No. US20050261218A1
GENERAL INFORMATION:
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXIEN=200000000 -USER=US10764259 @CGN 1 1.184 @runat_05122005_094549_7109
-MXXIEN=2000000000 -USER=US10764259 @CGN 1 1.184 @runat_05122005_094549_7109
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-LONGLOG -DEV TIMBOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 37665, A
Sequence 37665, A
Sequence 37096, A
Sequence 62270, A
Sequence 2510, A
Sequence 2501, Ap
Sequence 2501, Ap
                                                                                                                                                                                                            December 9, 2005, 10:37:52; Search time 248 Seconds (without alignments) 461.288 Million cell updates/sec
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3: /cgn2 6/ptodata/2/pubpna/USO7 NEW PUB.seq:*

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Copyright (c) 1993 - 2005 Compugen Ltd
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Listing first 45 summaries
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Perfect score:
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93
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Database

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Modulation

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PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
                                                                                                                                                                          CGGACGCTGTGCGAGAAAGGCAAAGGAAATTTTAACAAAAGAATCAAATGTGCAAGAGGTT 165
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                                                                                                                                                               6 AspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGluLeuGluVal
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248
34
19
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 814 LENGTH: 1541
                                                                        1.5e-171
1411.00
93.69%
82.39%
84.49%
                                                                               Percent Similarity:
Best Local Similarity: (Query Match:
                          TYPE: DNA
CRGANISM: H. sapiens
US-10-909-125-814
                                                                 Alignment Scores:
Pred. No.:
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		US/10750185 C. TIONS FOR INPERRING BOVINE TRAITS US/10/750,185 S 60/437,482 3.1 3.1	Length: 3342 Matches: 64 Conservative: 29 Mismatches: 80 Indels: 89 Gaps: 8	-185-59362 (1-3342)	rh 75	CACGGTCAATTCTAGATGCTACCACGTGCTTTAGAACTGAGGGGGAAAGA: [T 1512 rAsnTyrLeuPheMetGlyAspTyrV; 31 87	ŭ	YTYTTYTSETVAIGIUThrValSerLeuLr Le 100 Le 100 Le 100 Le Le Le Le Le Le Le Le Le Le Le Le Le	ubysvalArgTyrArgAspArg1leThr11eLeuArgGlyAsnHisGluS       [1 120           : : :		LeuileG [1 16	CACTGGTC 17	GIY-GIyLeuSerProSerLeuAspThrLeu 3A 178 GGTPACCTACTTCACAAACACCACCACCTCCTG 3A 1847	
286 PheGluProAlaProAr    :::          886 TTTGACCCGGCGCCTCG	306 Leu 306     946 CTA 948	Application US2005026060 US2005026060 GENOMICS, IN MISE, Sue K. Richard SENFELD, Davis, Tom TIS, Stephen NTIN, Dennis TION, COMPOSITION NUMBER: UMTILLON UMBER: UDATE: 2003-110N NUMBER: UD NOS: 64922 ILD NOS: 64922 ULIN Version ine 19866880	t Scores: 0.00451 .: 111.50 Similarity: 44.294 al Similarity: 30.484 tch: 6.684	259-13 (1-306) x US-10	26	453 CACGGTCAATTCTAGATGCTAC 75 rAsnTyrLeuPheMetGlyAsp		87 yTyrTyrSerValGluThrVal :::       ::: 573 GCCTGTAACACAGGAAACCCTG	100 uLysValArgTyrArgA  ::: 1633 TAGAGGGTCAGAATTAG	120 eThrGlnValTyrGlyPheTyrAspGluCys 	0		160 ePheCysLeuHisGly-	1
oy.	Oy Dp	RESULT 2 US-10-750-185-593 US-10-750-185-593 Sequence 59367, PUBLICATIONNO, GRENERAL INFORMA APPLICANT: MAI APPLICANT: NO APPLICANT: NO APPLICANT: RO APPLIC	Alignment S Pred. No.: Score: Percent Sim Best Local, Query Match	US-10-764-		4 8 8	D 1	OY Db	Qy Db	Qy Db		Db 1	oy Dp	

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Sequence 62270, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAINTER, Richard
APPLICANT: RERRY, Richard
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PATENTIN Version 3.1
                                                             APPLICANT: HOLM, TOTAL APPLICANT: HOLM, TOTAL APPLICANT: HOLM, TOTAL APPLICANT: HOLM, TOTAL APPLICANT: APPLICANT: Stephen APPLICANT: PANTIN, Dennis; TITLE OF INVENTION: COMPOSITIONS FOR INPERRING BOVINE TRAITS (TILE REFERENCE: MAIL100-2 US/10/750,185; CURRENT FILING DATE: 2003-12-31; PRIOR PAPLICATION NUMBER: US 60/437,482; PRIOR FILING DATE: 2002-12-31; NUMBER OF SEQ ID NOS: 64922; SOFTWARE: PatentIN version 3.1; SEQ ID NO 37066; LENGTH: 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 GlyGlnPheHisAspLeuIleGluLeuPheArgIleGlyGlyLysAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       962 GGCCAGTTCTATGACCTCCTGAACATATTTGAGCTCAACGGTTTACCCTC
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Mismatches:
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Matches:
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; ORGANISM: Bovine 19866880123096
US-10-750-185-62270
                                                                                                                                                                                                                                                                                                                                                                                                   19866880767627
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                   KERR, Richard
ROSENFELD, David
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86.36%
72.73%
5.57%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-750-185-37096
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                                                                                                                                                           217 PheGlyGlnAspIleAlaGluGlnPheAsnHisThrAsnGlyLeuSer-LeuValAlaAr 236
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                                                                  SerAspPro---AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThr 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: FARR, Richard
APPLICANT: Hold, Tom
APPLICANT: Hold, Tom
APPLICANT: Hold, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
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APPLICANT: GOODS:
APPLICANT: HOLM, Tom
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APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: APPLICANTION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PATENTIN Version 3.1
SEQ ID NO 37665
LENGTH: 1964
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Matches:
Conservative:
Mismatches:
Indels:
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|1018 AAAATAAAGTATTCAGAACGCGTA------
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US-10-750-185-37665
; Sequence 37665, Application US/10750185
; Publication No. US20050260603A1
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APPLICANT: MMI GENOMICS, INC.
                   1848 CAGTCCTGGATCTTTTTTGAGGC----
                                                                                                                                                                                                                                                                                    2006 CGTTCACCCACTTGCCCTGGAG 2027
                                                                                                                                                                                                                                                      236 gAlaHisGlnLeuValMetGlu 243
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Query Match:
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Pred. No.:
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US-10-764-259-13 (1-306) x US-10-750-185-62270 (1-1861)

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; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2501
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US-10-467-657-2503/c
                                                                   Alignment Scores:
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                                     1636 TTTTATGACCTTTGTGAACTGTTCAGAACTGGAGGTCAGGTTCCTGACACAAAACTACATA 1695
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                                                                                                                                                              Sequence 37667, Application US/10750185

Sequence 37667, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION.

APPLICANT: MAI GENOMICS, INC.

APPLICANT: BORISE, Sue K.

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: PANTIN, Dennis

TILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MAILION-2

CURRENT PAPLICATION NUMBER: US/10/750,185

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR PILING DATE: 2003-12-31

PRIOR PELING DATE: 2002-12-31

PRIOR PELING DATE: 2002-12-31

SOFTWARE: PatentIN version 3.1

SEQ ID NO 37667

LENGTH: 728

THENCH APPLICATION OF THE STATES

SEQ ID NO 37667

LENGTH: 728
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Publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FOUTANA Maria Rita
APPLICANT: FOUTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Eliaabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: 12003-08-11
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PAPLICATION NUMBER: GB-0103424.8
PRIOR PAPLICATION NUMBER: 201-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTHARE: SEQUING Version 1.04
SEQ ID NO 2501
LENGTH: 828
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; ORGANISM: Bovine 19866880838231
US-10-750-185-37667
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APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MISSIGNAI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
FILE REPERENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
  828
52
22
69
65
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                   US-10-764-259-13 (1-306) x US-10-467-657-2501 (1-828)
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  0.684
87.50
35.58%
25.00%
5.24%
                                         Percent Similarity:
Best Local Similarity:
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 3553
LENGTH: 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 ValSerLeuLeuValAlaLeuLysValArgTyrArgAspArgIleThrIl
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Publication No. US2005025557A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TEDELICANT: SMITHKLINE BEECHAM CORPORATION:
APPLICANT: SMITHKLINE BEECHAM D.1.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFRENCE: GF50013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR PILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: ECT/US01/04703
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
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PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
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US-11-135-855-18
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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LENGTH: 753
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; Sequence 3553, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: MERR, Richard
; APPLICANT: RERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
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; PRIOR FILING DATE: 2001-02-12; NUMBER OF SEQ ID NOS: 9218; SOFTWARE: SegWin99, version 1.04; SEQ ID NO 2503; LENGTH: 963; TYPE: DNA; ORGANIGM: Neisseria gonorrhoeae US-10-467-657-2503
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Matches:
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Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

Score: 87.00 Matches Percent Similarity: 35.63% Conserv Best Local Similarity: 23.08% Mismatc Query Match: 5.21% Indels: DB: 7 Gaps: US-10-764-259-13 (1-306) x US-11-121-086-66 (1	Oy 24 GluvalLysAsnLeuCysAspGlnAlaArgTh         : :   : :	152039 80 152090 152135 120 152186	Oy 140 TrpLysTyrPheThrAspLeuPheAspTyrLe  Db 152201 TGG	Db 152355 GGCTAC
US-10-764-259-13 (1-306) x US-11-135-855-18 (1-753)  Qy	Db 142 ATCCCTGGAAGGACTGCTGCACCTCACGACAAGCTGGAA 189  Qy 146 LeuPheAspTyrLeuProLeuThrAlaLeu1leGluHisGluIlePheCysLeuHisGly 165  :::	Qy 186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGly 205	Db 460CGTGGTGGCTGGGACTCGGGAAGAAC	RESULT 11 US-11-121-086-66  Sequence 66, Application US/11121086  Publication No. US20050266459A1  GENERAL INFORMATION:  APPLICANT: POULSEN, TIM S.  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  FILE REFERENCE: 09138.6000-00000  CURRENT APPLICATION NUMBER: US/11/121,086  CURRENT PELING DATE: 2005-05-04  PRIOR PILING DATE: 2005-05-04  NUMBER OF SEQ ID NOS: 107  SOFTWARE: Patentin version 3.3  SOFTWARE: Patentin version 3.3  TYPE: DNA  ORGANISM: Homo sapiens  US-11-121-086-66  Alignment Scores:  2.45e+03 Length: 163162

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Matches: 57 Conservative: 31 Mismatches: 74 Indels: 87 Gaps: 13	(1-163162)	GluGlu	: :	yAspileHisGlyGlnPheHi: 	-GTGTGAGCGCACAAACACGCATGGGAAAG,	OASPThrAs:	actccaacggccaacgr	<pre>MetGlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLe :::</pre>	-GCTTTGAGCACATGACTTCT	rIleLeuArgGlyAsnHisGl	ATGTCGCTACCTGCAAATGGGGAGGAAACTGTCTCACAGGGTAATCATGA	eThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAs)		rLeuProLeuThrAlaLeuIl	)LD	yLeuSerProSe:	GTCATCTGTCAAATGTAGGTCCCTGGGAAGGTCAATAAGCAATCTCCATC	LeuAspHisIleArgAlaLeuAspArgIleGlnGluValProHisGluGl:	CCCCAC	gCysGlyTrpGlyIleSerPr	AACATGCTCAGGCCCCAGCCAAGTGCCAAGCTGGGGTGGTGTCC	aGluGlnPheAsnHisThrAsnGl:		ValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAs	ATGGCCAGAGGTCC-AGGCTCAGGAGACTGGTTAGGGATGGTGAGTG			5 INFERRING BOVINE TRAITS
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Score: Percent Similarity: Best Local Similari Query Match: DB:	-10-764-259	Ň (		44	151982	64	152039	80	152090	100	152135	120	152186	140	152201	160	152216	174	152276	194	152297	214	152355	234	152361	254	152420	RESULT 12 US-10-750-185- ; Sequence 534; Publication; GENERAL INPC APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT; APPLICANT;
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US/10/750,185 12-31 5 60/437,482 3.1 896783	Length: 2348 Matches: 40 Conservative: 19 Mismatches: 61 Indels: 31 Gaps: 7	US-10-750-185-53466 (1-2348)  ysValArgTyrArgAspArgIle	CTTTTATGTTTAGAAAAAAGATACAGGCAAAGAAATGAAGAATGAGCTTTGTACCATCATC ArgGlyAsnHisGluSerArgGln-IleThrGlnValTyrGlyPhe	TyraspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLys	-TyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeulleGluHisGluIlePh 	eCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle 	ArgAlaLeuAspArgIleGlnGluValProHisGluGlyProMetCysAs 	y	PheGlyGln 219     :: CTGGGAAGG 135	Đ.
ENCE: MMI1100-2 PLICATION NUMBER: LING DATE: 2003- ICATION NUMBER: UG DATE: 2002-12- SEQ ID NOS: 64922 SEQ ID NOS: 64922 846 Bovine 19866880 53466	Scores: 5.22 86.00 milarity: 39.07 i Similarity: 26.49 th:	1	576 CTTTTATGTTTAGAAAAAAGAT 112 ArgGlyAsnHisGluSerArgG 516	TyrA		161 eCysLeuHisGlyGlyLeuSerProSerLeuAspThrL 	178ArgAlaLeuAsp     ::: 285 TGGAGGCCAAAATGCCCACAAG	194 pleuleuTrpSerAspProAspAspArgCysGl. 	209 rProArgGlyAlaGlyTyrThrPheGlyGln  :::    165 TTCTAAAGGTGTCAACAGAAAACTGGGAAGG	SULT 13 -10-955-054A-137 Sequence 137, Application US/10955054A Bebblication No. US20050266420A1 GENERAL INFORMATION: APPLICAMT: PUSZTAI, LAJOS APPLICAMT: SYMANS, W. FRASER APPLICAMT: SYMANS, W. FRASER APPLICAMT: SYMANS, W. FRASER APPLICAMT: STEC, JAMES TITLE OF INVENTION: MULTICENE PREDICTORS OF RESPONSE FILE REFERENCE: UTXC:880US TITLE OF INVENTION: MULTICENE 12/10/955,054A CURRENT APPLICATION VMDER: US/10/955,054A CURRENT APPLICATION VMDER: 2004-09-30 NUMBER OF SEQ ID NOS: 195 SOFTWARE: PATENTING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 195 SEQ ID NO 1337 LENGTH: 2401
FILE REFER  CURRENT FI  CURRENT FI  FRIOR APPL  PRIOR FILI  NUMBER OF  SOFTWARE:  SEQ ID NO 5  LENGTH: 2  LENGTH: 2  CORGANISM:  US-10-750-185	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match:	US-10-764-259 Qy 97	6 6 6		Oy 1	Qy 1	Oy 1	Oy 1 Db 2	Oy 2 Db 1	RESULT 13 US-10-955-054A-137 ; Sequence 137, Appl ; Publication No. US; GENERAL INFORMATIC; ; APPLICANT: BVSZTY ; APPLICANT: BVSZTY ; APPLICANT: SYMM; ; APPLICANT: SYMM; ; APPLICANT: SYMM; ; APPLICANT: SYMM; ; APPLICANT: SYMM; ; APPLICANT: SYMM; ; TITLE OF INVENTIC; ; TITLE OF INVENTIC; ; TURENT APPLICATIC; ; CURRENT FILLING DF; ; CURRENT FILLING DF; ; CURRENT FILLING DF; ; SEQ ID NO 137 ; LENGTH: 2401

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0y   110 e	Qy 134 rGlyAsnAlaAsnValTrpLysTyrPheThrAspLeuPheAspT.		Oy 255 rValPheSeralaProAsnTyr	Oy 302 0 302  Db 2226 C 2226  RESULT 15  US-11-121-086-13 ; Sequence 13, Application US/11121086 ; Publication No. US2050266459A1 ; General INFORMATION: ; APPLICANT: POULSEN, TIM S. ; APPLICANT: POULSEN, TIM S. ; APPLICANT: POULSEN, KIRSTEN V. ; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALK ; FILE REFERENCE: 09138.6000-00000 ; CURRENT FILING DATE: 2005-05-04 ; PRIOR FILING DATE: 2004-05-04 ; PRIOR FILING DATE: 2004-05-04 ; NUMBER OF SEQ ID NOS: 107 ; SOFTWARE: PATCHINI VERSION 3.3 ; SEQ ID NO 13 ; LENGTH: 191797 ; TYPE: DNA ; ORGANISM: Homo sapiens US-11-121-086-13
Qy         255 rValPheSerAlaProAsnTyr	282 rPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 2307 CATGCAGCTGGAAGAGCAGCTAGCAGAAATAAGCAGCAAGAAACGGCC 302 o 302	SULT 14 5-10-95-054A-1 6-10-95-054A-1 Fublication NG GENERAL INFORM APPLICANT: FAPPLICANT: FAPPLICANT: FAPLICA	mo sapiens 01 : 18.7 Length: 82.50 Matches ty: 37.12% Conservarity: 18.84% Mismatc 4.94% Indels: 6 Gaps:	US-10-764-259-13 (1-306) x US-10-955-054A-101 (1-2740)  OY 4 TYRALAASPVALASPARGGINILGGIUGINLEUSERGIUCYSLYSPFOLEUSERGIULEU 23  DY 24 GIUVALLYSASTCTCTCCTCCTGAA-GAATCAACCTGCTACCGGAAGTT 1232  OY 24 GIUVALLYSASTCTATGTGACATTCTTCGAGATCTACCACTTGACCTGCT 1292  OY 3 DFTOVALLYSCYSPFOVALTHRVALCYSGLYASPCATGGAAGCTGTTTGACCTGCT 1292  OY 43 nProVallySCYSPFOVALTHRVALCYSGLYASPCATGGAAGCTGTTTGACCTGCT 1292  OY 56 SGLYGINPheHis

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	126 PheryraegGluCysLeuargLysTyrGlyasnalaasnValTrpLysTyrPheThr 144	145 AspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluHisGluHePheCysLeuHis 164	165 GlyGlyLeuSerProSerLeuAspThrLeuAspHislleArgAla-LeuAspArglleGl 184 	184 nGluValPro 191 ::	192MetCysAspLeuLeuTrpSerAspProAspAspArgCy 204 ::    154982 AAATTAAGCCTTCTTCCCAAGCATCTGGTGCCATAGCCATAGCTTCTTTTGAATG 155041	204 sGlyTrpGlylleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspileAlaGluGl 224	nPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGl         :::      GTTTAACAGAAGCTT-GGCCCCAGACATGG	244 YTYrAsnTrp		
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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Q9mb06 vicia faba
Q6vuq6 lycopersico
Q9fsv3 fagus sylva
Q07098 arabidopsis
Q9mb05 vicia faba
Q8law8 arabidopsis
Q9ze4 hevea brasi
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DYLPLTALIEHEIFCLHGGLSPS            DYLPLTALIESQIFCLHGGLSPS	YYSVETVSLLVALKVRYRDRITI 	ELEVKNICDQARTILVEEWNVQPVKCPVI   :	e 1548; DB 2; Length 306 . No. 4.2e-129; ismatches 12; Indels	PRT; 306 AA.  PRT; 306 AA.  set sequence update) st sequence update) st smotation update) sic subunit.  o.  o.  1.365-313X.2004.02073.x; Solanaceae; Solanum; Lycopers  Solanaceae; Solanum; Lycopers  o., Gu YQ., Tang X., Marti rotein phosphatase 2A catalyt defense responses and locali phoprotein + H(2)O = a protei phoprotein phosphatase family.  mRNA.  tivity; IEA. se. apaH.  phatase; UNKNOWN_1.  C0719F26F8FCAOE5 CRC64;	MENTS	UMAN Q619t RARE 07zve RARE 07zve CK 07zve CK 07skgt NOGA 07pd3 E P2365 AN P6271 SE P6271 IT P6271 UMAN 08wz5 UMAN Q861k RARE Q661k RARE Q661e
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SMART; SM00156; PP2AG; 1.
PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
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Vicia faba (Broad bean).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Type 2A protein phosphatase-1.
Name=vfPP2Ac-1;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence
05-JUL-2004 (TrEMBLrel. 27, Last annotati
Protein phosphatase 2A catalytic subunit.
Name=PP2Ac1;
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ProDom; PD000252; T_phtase_apaH;
SMART; SM00156; PP2Ac; 1.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache-
Spermatophyta; Magnoliophyta; eudicotyledona; core eudicoty-
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopers
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SEQUENCE
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CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protei:
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306 AA;
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ilarity 91.2%;
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Pred. No. 7.4e-128;
2; Mismatches 15;
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Matches 274
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-!- SIMILARITY: Belongs to the PPP phosphatase family.

REMBL; AJ298829; CACI1129.1; -; mRNA.

R HSSP; P36873; 1JK7.

R GO; GO:0016787; F:hydrolase activity; IEA.

R InterPro; IPR004843; M-pesterase.

R InterPro; IPR006186; T_phtase apaH.

PFAm; PF00149; Metallophos; 1.

R PFAm; PF00149; Metallophos; 1.

R PFAM; PR000114; STPHPHTASE.

R PRINTS; PR000114; STPHPHTASE.

R PRODOM; PD000252; T_phtase apaH; 1.

SMART; SM00156; PP2AG; 1.
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1_ARATH STANDARI
07038,
01-OCT-1994 (Rel. 30, C
01-OCT-1994 (Rel. 30, I
13-SEP-2005 (Rel. 48, I
Serine/threenine protei
(EC 3.1.3.16).
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Name=PP2A1; OrderedLocusNames=At1g10430; ORFNames=T10024.4; Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gonzalez M., Nicolas C., Submitted (OCT-2000) to t
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01-MAR-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fagales; Fagaceae; Fagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMEGFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENMDQNFLQFDPAPRQIEPDTTRK
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89.5%; Pred. No. 3.8e-127;
tive 18; Mismatches 14; Indels
                                                                                                     Last sequence update)
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ein phosphatase PP2A-1 c
                                                                                                                                                                                       Created)
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A phosphoprotein + H(2)O = a protein +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088 Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Chan Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Chan Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G. Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Tor A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Tor A Miranda M., Guach H.L., Tripp M., Chang J.M., Akiyama K., A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carr Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hanse A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Kar Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai A, Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sa Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                  phosphate.
-:- COPACTOR: Binds 1 iron ion per subunit (By similarity)
-!- COPACTOR: Binds 1 manganese ion per subunit (By simila-
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the PPP phosphatase family. PP-
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STRAIN=cv. Columbia GL1;
MEDLINE=93184204; PubMed=8382968;
MEDLINE=93184204 PubMed=8382968;
This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no rest use as long as its content is in no way modified and this to the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the st
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Science 302:842-846(2003).
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InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; 1.
PRINTS; PR00114; STPHPHTASE.
ProDom; PD000252; T_phtase_apaH; 1.
SMART; SM00156; PP2Ac; 1.
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                                  phosphate.
-i-SIMILARITY: Belongs to (
EMBL; AB039917; BAA92698.1;
HSSP; P36873; 1JK7.
GO; GO:0016787; F:hydrolase
                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.

Ueno H., Kinoshita T., P
Submitted (MAR-2000) to
-!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; VicBI_TaxID=3906;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Type 2A protein phosphatase-2.
Name=vfPP2Ac-2;
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Hydrolase; Iron; Manganese;
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Q9MB05;
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                           F:hydrolase activity;
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Pred. No. 8.7e
17; Mismatches
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RESULT 7

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DT 01-OCT-2002 (TYEMBLEE1 26,
DT 01-MAR-2004 (TYEMBLEE1 26,
DT 01-MAR-2004 (TYEMBLEE1 26,
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DT 01-MAR-2004 (TYEMBLEE1 26,
DT 01-MAR-2004 (TYEMBLEE1 26,
DT 01-MAR-2004 (TYEMBLEE1 26,
DE Serine/threonine protein pho
OS Arabidopsis thaliana (Mouse
OC rosids; eurosids II; Brassi
OX NCBITAXID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22088475; PDAMMed=12
RA Hass B.J., Volfovsky N., To
RA Feldmann K.A., Flavell R.B.
RT "Full-length messenger RNA
RT Genome Biol. 3: RESEARCH0029
RN [2]
RN UCLEOTIDE SEQUENCE.
RA BROVER V., TTOUKHAN M., Ale.
Feldmann K.;
RI Genome Biol. 3: RESEARCH0029
RN NUCLEOTIDE SEQUENCE.
RA BROVER V., TTOUKHAN M., Ale.
Feldmann K.;
CC 1- CATALYTIC ACTIVITY: A p
CC 1- CATALYTIC ACTIVITY: A p
CC 1- SIMILARITY: Belongs to
DR EMBL; AY087557; AAM65099.1;
DR HSSP, P56873; 1176.
DR EMBL; AY087577; F: hydrolase
DR InterPro; IPR0061843; M-pest
DR Ffam; PF00149; Metallophos;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyrosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; 1.
PRINTS; PR00114; STPHPHTASE.
ProDom; PD000252; T_phtase_apaH; 1.
SMART; SM00156; PP2Ac; 1.
SMART; PS00155; SER_THR_PHOSPHATASE; UNKNOWN_1.
PROSITE; PS00155; SER_THR_PHOSPHATASE; UNKNOWN_1.
                                                NUCLEOTIDE SEQUENCE.

MEDLINE=22088475; PubMed=12093376;
Haass B.J., Volfovsky N., Town C.D., Tro
Feldmann K.A., Flavell R.B., White O.,
"Full-length messenger RNA sequences grannotation.";
                                                                                                                                         Submitted (MAR-2002) to the -I- CATALYTIC ACTIVITY: A pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Serine/threenine protein phosphatase type 2A, putative.
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SEQUENCE
     InterPro; IPR004843; M-pesterase.
InterPro; IPR006186; T_phtase_apaH
Pfam; PF00149; Metallophos; 1.
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larity 89.9%;
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0527K2 ORYSA
0527K2;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TremBLrel. 28, Last annotation update)
25-OCT-2004 (TremBLrel. 28, Last annotation update)
25-OCT-2004 (TremBLrel. 28, Last annotation update)
25-OCT-2004 (TremBLrel. 28, Last annotation update)
26-OCT-2004 (TremBLrel. 28, Last annotation update)
27-OCT-2004 (TremBLrel. 28, Last annotation update)
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26-OCT-2004 (TremBLrel. 28, Last sequence update)
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                                                            PROSITE; PS
Hydrolase;
SEQUENCE
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,
clone:OSJNBB0006A22.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a pro
                                                                                                                                                                                                                                                                                                                                               phosphate.
--- SIMILARITY: Belongs to the EMBL; AP004729; BAD61854.1; -; Gramene; OSZ7K2; ---
                                                                                                                                               GO; GO:0016787; F:hydrolase activity;
InterPro; IPR004843; M-pesterase.
InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; 1.
PRINTS; PR00114; STPHPHTASE.
ProDom; PD000252; T_phtase_apaH; 1.
SMART; SM00156; PP2AC; 1.
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ProDom; PD000252; T_phtase_apaH; 1.

SMART; SM00156; PP2AG; 1.

PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
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                                                                                                                   PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
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306 AA; 34934 MW;
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                                                            35113 MW;
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   90.5%;
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Pred. No. 4.5e
17; Mismatches
   Score 1512; DB 2;
                                                                                                                                                                                                                                                                                                                                                                          PPP phosphatase Genomic_DNA.
                                                         F95722F8A638FF31 CRC64;
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4.5e-126;
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0925E4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine protein phosphatase PP2A cat
                       EMBL; AF107464; AAD09953.1; -; mRNA
HSSP; P08129; 1FJM.
InterPro; IPR004843; M-pesterase.
InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; 1.
PRINTS; PR00114; STPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Shin D.H., Han K.-H.;
"Isolation of a cDNA encoding a type 2A serine/threonine
"Isolation of a cDNA encoding a type 2A serine/threonine
phosphatase (PP2A) from Hevea brasiliensis.";

(er) Plant Gene Register PGR99-011.

-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hevea brasiliensis (Para rubber tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
rosids; eurosids I; Malpighiales; Buphorbiaceae; Crotonoide
Micrandreae; Hevea.
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                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3981;
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as long a
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                                                                                                                                                                                                                         Swiss-Prot entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Elevropean Bioinformatics Institute. There are no rest
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P2A3 ORYSA

STANDARD;

PRT;

OYSGT7;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

13-SEP-2005 (Rel. 48, Last annotation update)
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STRAIN-CV. Indica / IR36;
YU R.M.K., Kong R.Y.C.;
YU R.M.K., Kong R.Y.C.;
"Molecular cloning and characterization of protein phosphatase catalytic subunit genes from Oryza sativa.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
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ACT_SITE
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Spermatophyta; Magnoliophyta; Liliopsid
Ehrhartoideae, Oryzeae, Oryza.
NCBI_TaxID=4530;
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COFACTOR: Binds 1 manganese ion per

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InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; 1.
PRINTS; PR00114; STPHPHTASE.
ProDom; PD000252; T_phtase_apaH; 1.
SMART; SM00156; PP2Ac; 1.
PROSITE; PS00125; SER_THR_PHOSPHATASE;
 Sasaki T.,
Submitted
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                                                                    Name=P0027A02.2-1;
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache-Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                       NUCLEOTIDE
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HSSP; P08129; 1FJM.
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EMBL/GenBank/DDBJ databases.
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Pred. No. 1.4e-125;
3; Mismatches 11;
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RESULT 12
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DT 01-0CT-1994 (Rel. 30, Created)
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Matches 272;
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STRAIN-cv. Columbia GL1;
MEDLINE=93184204; PubMed=8382968;
MEDLINE=93184204; PubMed=8382968;
                                                                                                                                                                                                                                  Name=PP2A2; OrderedLocusNames=At1g59830; ORFNames=F23H11.15; Arabidopsis thallana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702;
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Gramene, Q6Z6L9; -.
GO; GO:0016787; F:hydrolase activity; InterPro; IPR004843; M-pesterase.
InterPro; IPR006186; T_bhtase_apaH.
Pfam; PF00149; Metallophos; 1.
                                                               "Protein phosphatases in higher plants: phosphatases in Arabidopsis thaliana."; Plant Mol. Biol. 21:475-485(1993).
                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threonine protein phosphatase PP2A-2 catalytic subunit
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SEQUENCE 307 A
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ProDom; PD000252; T_phtase_apaH;
SMART; SM00156; PP2AC; 1.
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SIMILARITY: Belongs to the PPP phosphatase family.
L; AP004996; BAD17174.1; -; Genomic_DNA.
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88.6%; Pred. No. 1.4e-125;
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WEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500; Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul White O., Alonso J., Altafi H., Arauje R., Bowman C.L., Brc Buehler B., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W. Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dunn P., Ergu P., Feddblyum T.V., Feng J.-D., Fong B., Fuji R. Gill J.E., Goldemith A.D., Haas B., Hansen N.F., Hughes B., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khayki Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., A. Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H., Li J.H.
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A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Ch
A Kariin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G
A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Tox
A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K.,
A Arakawa T., Bahh J., Banno F., Bowser L., Brooks S.Y., Carr
A Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hanse
A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Kar
A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai
A Kaniya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sa
Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.
Tempirical analysis of transcriptional activity in the Arah
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M96732; AAA32847.1; -; mRNA.

EMBL; AC007258; AAD39326.1; -; Genomic_DNA.

EMBL; AY063942; AAL36298.1; -; mRNA.

EMBL; AY096543; AAM20193.1; -; mRNA.

PIR; S31161; S31161.

HSSP; P36873; 1IT6.

InterPro; IPR006186; T_phtase_apaH.

Pfam; PF00149; Metallophos; 1.
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ProDom; PD000252; T_phtase_apaH; 1.

SMART; SM00156; PEDAG; 1.

PROSITE; PS00125; SER THR_PHOSPHATASE; 1.

Hydrolase; Iron; Manganese; Metal-binding; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are r
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HSSP; P08129; 1FJ
Gramene; Q9ZSS3;
InterPro; IPR0048
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NUCLEOTIDE SEQUENCE.

STRAIN=cv. Indica / IR36;

Yu R.M.K. / Zhou Y., Xu P., Kong R.Y.C.;

Yu Round and characterization of a rice gene encoding a catalytic subunit of protein phosphatase 2A.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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COPACTOR: Binds 1 iron ion per subunit (By similarity).

COPACTOR: Binds 1 manganese ion per subunit (By similarity)

COFACTOR: Binds 1 manganese ion per subunit (By similarity)

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: Belongs to the PPP phosphatase family. PP-2A
                                                                                                                                                                     European
                                                                                                                                                                   Swiss-Prot entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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       IPR004843; M-pesterase.
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Last annotation update)
ein phosphatase PP2A-1 catalytic subunit
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Pred. No. 1.5e-125;
7; Mismatches 17;
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Manganese (By similarity).
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Best Local Similarity
Matches 268; Conserv
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P48579;
01-FEB-1996
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SEQUENCE
                                                                                                                                                      Helianthus annuus (Common sunflower).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty

asterids; campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.
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PROSITE; PS00125; SER THR PHOSPHATASE; 1.

Hydrolase; Iron; Manganese; Metal-binding; Multigene family
                                              NUCLEOTIDE SEQUENCE:
TISSUE=Root meristem;
MEDLINE=5339397; PubMed=7664759;
MEDLINE=5339397; PubMed=7664759;
Menzel D., Vugrek O., Frank S., Elsner-Menzel C.;
"Protein phosphatase 2A, a potential regulator of actin-based organelle motility in the green alga;
Eur. J. Cell Biol. 67:179-187(1995).
                                                                                                                                                                                                                    Serine/threonine protein (EC 3.1.3.16).
                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Serine/threemine protein phosphatase PP2A cat
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ACT_SITE 115 1
METAL 54
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Pfam; PF00114; Metallophos; 1.
PRINTS; PR00114; STPHPHTASE.
PRIDOm; PD000252; T_phtase_apaH; 1.
                                                                                                                                            NCBI_TaxID=4232;
                                    -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0
            phosphate.
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Manganese (By similarity).
Manganese (By similarity).
Manganese (By similarity).
Manganese (By similarity).
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Pred. No. 2.3e
25; Mismatches
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  per subunit
                                                          regulator of
e green alga A
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AC 00495
DT 16-OC
DT 13-SE
DE Serin
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GN Name=
OC Sperm
OC Sperm
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Best Local S
Matches 270
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004951; 042544;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

Serine/threonine protein phosphatase PP2A-5 catalytic subunit
Name=PP2A5; OrderedLocusNames=At1g69960; ORFNames=F20P5.30, T17F3... Arabidopsis thaliana (Mouse-ear cress). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; 1.
PRINTS; PR00114; STPHPHTASE.
ProDom; PD000252; T_phtase_apaH; 1.
SMART; SM00156; PP2AC; 1.
PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use as long as its content is in no way modified and this statement is no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                           (EC 3.1.3.16).
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Pred. No. 5.8e
21; Mismatches
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Score 1495; DB 1; Pred. No. 2.2e-124;

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DR PFONDOM; PR00114; STPHPHTASE.

DR PRODOM; PD000252; T_phtase apaH; 1.

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Stamey R.T., Rundle S.J.;
Stamey R.T., Rundle S.J.;
Characterization of a novel isoform of a type 2, protein phosphatase from Arabidopsis thaliana.";
protein phosphatase from Arabidopsis thaliana.";
(er) Plant Gene Register PGR95-116.
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-!- COPACTOR: Binds 1 manganese ion per subunit (By similar-
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the PPP phosphatase family. PP-2
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EMBL; AC002062; AAB61116.1; -; Genomic_DNA.
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                 - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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TION ION N DS	ORGANISM Physcomit: Eukaryota Bryopsida REFERENCE 1		BASF Plan FEATURES Source		Alignment Scores: Pred. No.: Score: Percent Similarity:	Best Local Similarity Query Match: DB:	1	1 Met Pros 		131 TCGGAGT 41 ABNValG 	191 AACGTGC 61 AspLeuI	251 GATCTCA	81 GlyAspT		371 AAGGIGC 121 ThrGlnV 	431 ACGCAAG	 491 AAGTACT	161 PheCysL 		201 GAICGIA 201 ABDABDA
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al Similarity: 100.00% Mismatches: 0 tch: 100.00% Indels: 0 Gaps: 0 4-259-13 (1-306) x AR606281 (1-1365)	1 MetProSerTyralaaspyalaspargGlnIleGluGlnLeuSerGluCysLysProLeu 20 	21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40 	41 AsnvalginprovallyscysprovalthrvalcysglyaspileHisGlyginPheHis 60 	61 AspieulleGluLeuPheArgileGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80 	81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100 	101   LysValArgTyrArgAspArg1leThrIleLeuArgGlyAsnHisGluSerArgGlnIle	ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLy8TyrGlyAsnAlaAsnValTrp		141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluHie 160	161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180 	AspArglleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro	611 GAICGIAITCAAGAAGIGCCGCACGAGGGCCCGAIGIGIGIGAICIACICIGGICIGAICCA 6/0 201 AsnasnardvaGlyfrnGlyflaSerProaraglyalaGlyfryhrphaGlyglnasn 220	GATGATGTTGTGGATGGGGGATTTCACCACGAGGTGCGGTTATACTTTTGGTCAAGAT	221 IlealagluglnPheasnHisThrAsnGlyLeuSerLeuValAlaArgalaHisGlnLeu 240 	241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260 	AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn	AATTACTGTTACCGCTGTGGGAACATGGCCGCCATAATGGAGATAGAT	281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300	301 ThrProAspTyrPheLeu 306 	AX490719 1365 bp DNA linear PAT 16-AUG-2002
Best Local Sir Query Match: DB: US-10-764-259	ζζ q <sub>Ω</sub>	ço qa	රු සි	ço qa	<u>خ</u> ۾	<i>∂</i> 8	8	qa	<u>\$</u> 4	ර සි	ठे व	9 8	g q	& <del>8</del>	දි සි	ò	qq ,	දු පු	8 %	RESULT 2 AX490719 LOCUS

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tent W00246442.  23691 ens ens lantae; Streptophyta; Embryophyta; lantae; Streptophyta; Embryophyta; dae; Funariales; Funariaceae; Physi nert, H.J., Ishitani, M., van Thielei- related proteins and methods of us GmbH (DE) Qualifiers ="Physcomitrella patens" ="Physcomitrella patens" ="taxon:3218"	Length: 1365 Matches: 306 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0	IS (I-300) X ANYSOLIS (I-1303) Met ProSerTyralaAspValaspArgGlnIleGluGlnLeuSerGluCy:	TCGGAGTTGCAGGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGGTC ASHVAIGINPEOVALLYSCYSPEOVALThEVALCYSGTYASPIleHisG1: AACGTGCAGCCCGTGAAGATCTACGGTTTGCGGTGACGATCCTTGGT AACGTGCAGCCCGTGAAGTGTCCTGTCACGGTTTGCGGTGACATCCTGTGGG	AspLeulleGluLeuPheArg1leGlyGlyLysAlaProAspThrAsnTy:	LygvalArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe:	LystyrPherhrAspLeuPheAspTyrLeuProLeuThrAlaLeu11eG1 AAGTACTTCACGATTCGACTACCTGCCTCTGACACTCTCATGAC AAGTACTTCACGATTCGACTACCTGCCTCTGACACTCTCATTGAC PheCysLeuHisG1yG1yLeuSsrProSsrLeuAspThrLeuAspHis11.
Sequence 8 from Patent W00246442. AX490719 AX490719.1 GI:22323691 Physcomitrella patens Physcomitrella patens Physcomitrella patens Bryopsida; Funariidae; Funariales; 1 a Costa, E.S., Bohnert, H.J., Ishiti Chan, R. Phosphatase stress-related protein Patent: WO 0246442-A 8 13-JUM-2002 BASF Plant Science GmbH (DE) Location/Qualifiers 1.165 /organism="Physcomitrella /mol type="unassigned DNA /db_xref="taxon:3218"	Mo.: 1.59e-160 .: 1670.00 .: 1670.00 .: 100.00\$ .: 100.00\$ .: Match: 6764-259-13 (1-306) x ax490719	1 h H H H			1-4 H-4	
DEFINITION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	N	н н	Oy 61 Db 251 Oy 81 Db 311	Oy 101  Db 371  Oy 121  Db 431	OY 141  Db 491  OY 161  Db 551  OY 181  OY 09

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lis 60 :: 'AC 486

eu 20 || TA 366

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eu 100 1d 606 1e 120 1c 666 3d 726

le 160 || TA 786

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Ì	GATGATGTTGTGGATGGGGCATTTCACCACGAGGTGCCGGTTATACTTTTGGTCAGAT 73	ORIGIN	,				
•	221 IleAlaGluGlnPheAsnfisThrAsnG.yLeuSerLeuValAlaArgAlaHisGlnLeu 240 	Alignment Pred. No.: Score:	int Scores: lo.:	5.2e-148 1548.00		1511 279	
•••	241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260 	Percent Simi Best Local S Query Match: DB:	ent Similarity: Local Similarity: / Match:	96.08% 91.18% 92.69% 15	Conservative Mismatches: Indels: Gaps:		
	AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 28	US-10-764	-259-	) x AY325818	(1-1511)	;	
- •	851 AATTACTGTTACCGCTGTGGGAACATGGCCCCCATAATGGAGATAGAT	& a	1 MetProSer'          307 ATGCCGTCT	TyrAlaAspValAe :::      :::   CATGCAGATCTAGA	MetProSerTyrAlaAspValAspArgGlnIleGluGlnfeuSerGluC           :::       :::	InLeuSerGluCy        ATTGATGGAGTC	
,	911 CGGTCTTTTCTTCAGTTCGAACCAGCACCGCGGCAAAGTGAACCAGATGTGACGCGGAAG 970 301 ThrproapTyrPheleu 306	<i>≿</i> 8	21 SerGluLeu(        367 TCGGAAGCT	GluValLysAsnLe :::       GATGTGAAACTC	ergluLeugluValLysasnLeuCysaspglnalaArgThrIleLeuVa 	aArgThrIleLeuVa        aAGGCTATACTTGT	
		ð f	41 Asnvalgln	ProvalLysCysPi		1yAspileHisGl 	
AY325818 LOCUS DEFINITION	AY325818 Lycopersicon esculentum protein phosphatase 2A catalytic subunit	3 & 8		GluLeuPheArgI	AspleulleGluLeuPheArglleGlyGlyLysAlaProAspThrAsnTy	roAspThrAsnTy	
ACCESSION VERSION	A7325818 A7325818.1 GI:34398262	8 &	81 GlyAspTyr	valAspArgGlyT)	resectorie (r.TyrServalGluT)	hrvalSerLeuLe	
KEYWORDS SOURCE OPGANIEM	Lycopersicon esculentum (Solanum lycopersicum)	qu	547 GGCGATTAT			CTGTCACACTTT	
	Properation escuelum Ebikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.	& 8	101 LysValArg'          607 AAGGTTCGT'	Tyrargasparg1]                  TataGaGataGaa	LysvalargTyrargasparg1leThr11eLeuargG1yAsnHisG1uSe 	lyasnHisGluSe 	
REFERENCE AUTHORS TITLE	1 (bases 1 to 1511) He,X., Anderson,J.C., Pozo Od,O., Gu,Y.Q., Tang,X. and Martin,G.B. Silencing of subfamily I of protein phosphatase 2A catalytic subunits results in activation of plant defense responses and	중 음	121 ThrGlnval'         667 ACCCAAGTG	TyrGlyPheTyrAe               TATGGTTTTTATG	ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl 	ysTyrGlyAsnAl 	
JOURNAL	localized cell death Plant J. 38 (4), 563-577 (2004)	λō	141 LysTyrPhe'	ThraspleuPheas	LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGl	hrAlaLeuIleGl	
REFERENCE AUTHORS	1.25.04 2 (bases 1 to 1511) He,X., Anderson,J.C., del Pozo,O., Gu,YQ., Tang,X. and	qa		ACTGATCTTTTG	ATTATCTACCACTAA(	CAGCACTGATAGA	
TITLE JOURNAL	Martin, G.B. Direct Submission Submitted (18-JUN-2003) Boyce Thompson Institute, Cornell	& 8	161 PheCysLeul	HisGlyGlyLeuSe 	PhecyslentisGlyGlyLeuSerProSerLeuAspThrLeuAspHis11 	hrLeuasphis1           :::   CaCTGGATAATAT	
FEATURES	University, Tower Road, Ithaca, NY 14853, USA Location/Qualifiers	Š	181 Aspargile	GlnGluValProHi	sGluGlyProMetC	ysAspLeuLeuTr	
source	11511 /organism="Lycopersicon esculentum" /m] t-v-no-"mDND."	ପ୍ଧ	847 GACCGTATA	CAAGAGGTTCCAC		GTGATCTCCTGTG	
gene	/w.r	<b>à</b> 4	201 AspAspArg          907 GATGATCGG	CysGlyTrpGlyI]                TGTGGTTGGGGAA	AspaspargCysGlyTrpGly1leSerProArgGlyAlaGlyTyrThrPh 	laGlyTyrThrPh	
5,177	/gene="PP2Ac2"	ìè		Clubbaanuian	raging w. Fem Seri	Tangelaland	
CDS	/gnne="PP2Ac2" 3071227	දු දි			ATAGCATCTCAATTCAATCACACCAATGGTCTCACCCTGATTTCTAGAGC	: : : : :	
	/gane="ptxAcz" /note="lePp2Acz" /codon_start=1	ò:		GlyTyrAsnTrpC)	ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh	alvalThrvalPh	
	<pre>/product="protein phosphatase 2A catalytic subunit" /protein da AAO(5226.1" /ar</pre>	අ දි		GGTTTCAATTGGTC	STCAGGATAAGAATG	TTGTGACAGTATT	
	/w_xre=-u_1:44 > 2.5.65 > 2.65 \ /translation="WPSHABLDENCHEQLEMECKPLSEADVKTLCDQARAILVEEWNVQP VKCPVTVCGDIHGQPYDLIELFRIGGNAPDTNYLFMGDYVDRGYYSVETVTLLVALKV	<del></del>	1087 AACTATIGE	17 FATGCY BG17AE 	ABILYTCYBYYATGGYBUTABINGELAAALIEGREUUTBABDOL 	ecgiuileaspoi ::       ragaaaraggcga	
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410	/gene="PP2Ac2"	& 	301 ThrProAsp	ThrProAspTyrPheLeu 306			

eu 240 || :TT 1026

.sp 220 || |AT 966

ro 260 || |CA 1086

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.sn 280

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41 76 76 76 76 76 76 76	121 ThrGlnValTyrGlyPheTyraspGluCysLeuArgLysTyrGlyAsnAli 616 ACTCAAGTGTATGGCTTCTACGAGAGTGCTTGAGAAATGC 141 LysTyrPheThrAspLeuPhcAspTyrLeuProLeuThrAlaLeu1leGl 676 AAATTCTTACGACTTGTTTGATTATTATTACCTCTGACCGCCTTATTGA 161 PhcCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHis1li 676 AAATTCTTTAGATGGAGTCTCTCGCCATTTTGAT 181 AspArg1leGlnGluValProHisGluGlyProMetCysAspLeuLeuTr 181 AspArg1leGlnGluValProHisGluGlyProMetCysAspLeuLeuTr 194 GATCGCATACAGGAGTTCCACATGAGACCGATGTGGATACTTTTGATGATACTTTTGATATTTTTTTT	201 AppaspArgCysGlyTrpGlylleSerProArgGlyAlaGlyTyThhPhi 856 GATGATCGTTGGGGAATATCTCCACGAGGTGCTGGATATACATT 221 IlealaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValalaArgAli 916 ATGCTGCCGTTCAATCATACAATGTCTCTCACTGATATCTGGGC 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPhi 976 GTGATGGAGATACATATACAAATGGTCTCTCACTGATATTATAGGC 261 ASHTYTCYSTYRAGCYSGLASMEtAlaAlaIleMetGluIleAspGli 1036 AATTACTGCTACCGATGGGGAATATGGCTGCGGAATTGGGGG 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa: 1156 AGACTAGCTACCGAGGTTGATGGCTGCGAATTGAGCCTGACAC 301 ThrProAspTyrPheLeu 306 1156 AGACCAGATTATTTTTG 1173	AY325817  Lycoperation esculentum protein phosphatase 2A catal; (PP2AC1) mRNA, complete cds. AY325817  AY325817. GI:34398260  Lycoperation esculentum (Solanum lycoperaticum)  Lycoperation esculentum  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core en asterids; lamidés; Solanales; Solanaceae; Solanum; L: 1 (bases 1 to 1380)  He, X., Anderson, J.C., Pozo Od, O., Gu, Y.Q., Tang, X. as Silencing of subfamily I of protein phosphatase 2A ci subbunits results in activation of plant defense respe
8 6 8 6 8 6 8	8686868		AY325817 LOCUS DEFINITION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE
Db 1207 ACTCCAGATTACTTTTG 1224  RESULT 4  AB039916 LOCUS LOCUS LOCUS DEFINITION Vicia faba vFP2Ac-1 mRNA for type 2A protein phosphatase-1,  COMPLETE CGS.  ACCESSION AB039916	Nicia.  Vicia.  AUTHORS  Uno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.  AUTHORS  TITLE  Type 2A protein phosphatase from guard cells of Vicia faba JOURNAL  Published Cally in DataBase (2000)  REFERENCE  C (bases 1 to 1417)  AUTHORS  Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.  TITLE  Direct Submission JOURNAL Submitted (108-AMR-2000)  TORNAL	/mol type="membra" /mol type="membra" /dev stage="mature" /dev stage="mature" /note="synonym:Vicia faba L." 11417 CDS /Gene="vfPP2Ac-1" 2561176 /gene="vfPP2Ac-1" /codon start=1 /product="type 2A protein phospha/protein id="BAA32697.1" /product="type 2A protein phospha/protein id="BAA32697.1" /product="type 2A protein phospha/protein id="BAA32697.1" /db_xref="dl:7A8359" /translation="meshableRQIEHIMECKEVCEOUNCEDINGUELMECKEVCEOUNCEDINGUELMECKEVCEOUNCEDINGUELMECKEVCEOUNCEDINGUELMECKEVCEOUNCEDINGUELMECKEVCEOUNCEDINGUELSIARAGINAPDTNY RYRDRITILRGNHESRQITOVYGFVDECLRKVG PCHIGGIGESSEJDTLDNIRALDRIGEPHEGPMC QDIAAGENHTWGLSLISRAHQINWEGFRWCGEP ENMDQNFLQFDPARQIEPDTTRKTPDYFL" //note="17 a nucleotides"	Score

le 160 || TA 749 ro 200 || |CA 869 ro 260 || CA 1049

eu 240 || |TT 989 AG 1109

sn 280

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241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh. [	SE PARCE		<b>υ</b>
8 6 8 6 8 6	RESULT 7 AV093267 LOCUS DEFINITION ACCESSION VERSION KEYWODS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOUIT Gene CDS
NIS	Alignment Scores:     Pred. No.:	yeAsnLeuCy8AspGlnAlaArgThrI	

cloned (7) as CA 780

Db   721 GTCATGGAAGGTTTTAACTGGTGTCAGGATAAGAATGTGGTGTGTTTTAACTGGTGTCAGGATAAGAATGTGGTGTTGTTTTAACTGGTGTCAGGATAAGAATGTGGTGTTGTTTAACTGGTGTCAGGATAAGAATGTGATGTTTGTT	RESULT 8 ATHPRPHB LOCUS DEFINITION Arabidopsis thaliana protein phosphatase mRNA, complacESSION M96733.1 GI:166822 KEYWORDS Protein phosphatase. KEYWORDS Arabidopsis thaliana (thale cress)	NISM NCE ORS	Diogent phosphatases in inguer plants: multiplicity phosphatases in Arabidopsis thaliana JOURNAL Plant Mol. Biol. 21 (3), 475-485 (1993) PUBMED 8382968  COMMENT Original source text: Arabidopsis thaliana (library:		/organism="Arabidopsis thaliana" /mol_type="mmkNa" /db xref="taxon:3702" /tissue_type="whole plant (including root)" /dev_stage="whole plant dincluding root"	/tissue llb="lambda GT10" 1181038 dephosphorylation of Ser-P and T /note="putative"	/codon_start=1 /product="protein_phosphatase" /protein_id="AAAA32848-1" /db_xref="G1:166823" /db_xref="G1:166823" /trānslation="mpsNGDLDRQIRQCKPLSEADVRTLC /krānslation="mpsNGDLDRQIRGCKPLSEADVRTLC VKCPTVCGDIHGQFYDLIBLERIGGNAPDTNYLFMGDYVDRG VKCPTVCGTHGGPYDLIBLERIGGNAPDTNYLFMGDYVDRG VKCPTVCGTHGGPYDLIBLERIGGNAPDTNYLFMGDYVDRG VKCPTVCGTHGGPYDLIBLERIGGNAPDTNYLFMGDYVDRG VKCPTVCGTHGGNAPDFCLRKYGNANVWKYFTD	CLHGGLESELDITABLESIDE LGEVERGEPMCDLLWSDEDDR QDIFAQFNIRNGLSIISRAHQIVWEGERWCQDRXVVTVFSAPN ENMEQNFLQFDPAPRQVEPDTTRKTFDYFL" ORIGIN	1.87e-145 Length: 1522.00 Matches:	Best Local Similarity: 90.10% Conservative: 17 Best Local Similarity: 90.54% Mismatches: 15 Query Match: 91.14% Indels: 0 DB: 15	-10-764-259-	OY I MECETOSETIYTALAMBYALAMBANGTHIJEGINUSHIGUSETGILUÇY   1
/gene="Atig10430" /codon_start=1 /product="similar to protein phosphatase type 2A" /protein id="Aam1266.1" /db_xref="Gia="Am1266.1" /db_xref="Gia="MPSNGDLDRQIEQIMECKPLSEADVRTLCDQARAIIVERYNVQP /translation="MPSNGDLDRQIEQIMECKPLSEADVRTLCDQARAIIVERYNVQP /translation="MPSNGDLDRQIEQIMECKPLSEADVRTLCDQARAIIVERYNVQP /translation="MPSNGDLGIECHTCGNAPDYLPTDLPDYLPYLLILISQV RYRDRITILRGNHESRQITQNYGPYBECIMKYGNNVWYPTDLPDYLPYLTILISQV FCLHGGISPSLDTLDNIRSLDRYDHEGREWCDLLWADPDDRCGWGISPRGAGYTFG QDIAAQFNHNNGLSLISRAHQLVWEGFWACQDRNVVTVFSAPNYCYRCGNWAAILEIG ENMEQNFLQFDPAPRQVEPDTTRKTPDYFL"	Alignment Scores: 1.55e-145 Length: 1092 Score: 1522.00 Matches: 274 Bercent Similarity: 95.10\$ Conservative: 17 Best Local Similarity: 89.54\$ Mismatches: 15 Query Match: 15 Gaps: 0 US-10-764-259-13 (1-306) x AY093267 (1-1092)	Qy         1 MetProSerTyralaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20           Db         1 ATGCCGTCGAACGGAGATCTGGACCGTCAGATCGAGCTGTATGAGGTGTAAACCGTTA 60           Qy         21 SerGluLeuGluValLysAsmLeuCysAspGlnAlaArgThrIleLeuValGluGrup 40	41 Asn 	Qy     61 AspLeulleGluLeuPheArgileGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80       Db     181 GACCTTATTGAGCTCTTTCGTATCGGGGAACGCTCCTGATACTAACTA	81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu	101 LysvalardfyrargaspargilefhrilefeuargGlyashHisGluSerArgGlnIle 	Cy         121 Thr61n041Tyr61yPhefyrAsp61uCyeLeuArgLysfyrG1VasnAlaAsnNa1Trp 140           bb         361 ACTCAAGTCTATGGTTTTTTTAGGAGGAGTTGGGAAATGCTAAGGTTCTGG 420           Cy         141 LysfyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeu1leG1uHisG1uHe 160           Cy         141 LysfyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeu1leG1uHisG1uHe 160           Db         421 AAGTATTTACAGACCTTTTCGATTATCTTCCTCTTACCGCCTCATAGAGAGTCAGGTT 480	Oy 161 PheCysLeuHisGlyClyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180	Oy 181 AspArgileGinGluValProHisGluGiyProMetCysAspLeuLeuTrpSerAspPro 200	Qy         201 AspAspArgCysGlyTrpGly11eSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp         220	Oy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240	241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValV

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l (bases 1 to 1343) Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kam: Kawai, J., Kim, C., Lin, J., Liu, S.X., Natusaka, M., Phar Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission Submitted (22-OCT-2001) DNA Sequencing and Technology Stanford University, 855 California Avenue, Palo Alte USA Genomic Sciences Center (GSC) members carried collection and clustering of RAFL cDNAs (RAFL cDNA : Arabidopsis Full-Length cDNA): Seki, M., Narusaka, M. Satou, M., Kami, Y., And Shinozaki, K.	The Salk, Stanford, PGEC (SSP) Consortium members casequencing and annotation of the RAFL CDNAs: Nguyen, I Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M. Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chui Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn Yamada, K., Ecker, J., Theologis, A. and Davis, R.W. Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contequally to this work. Shinozaki, K. (RIKEN GSC) and I (SSP/Stanford) contributed equally to this work as i	e Scores: milarity: Similarity	1 Met ProSerTyralaAspValAspArgGlnileGluGlnLeuSerGluCy;
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ୂ ଓ ୧ ନିଛନ୍ତ ନ ସହର ସିଥିୟର ଜିତି ହିନ୍ଦି ।	ASPARGILEGINGIUVAlProHisGluGlyProMetCysAspleuLeuTrpSerAspPro 2 GATCGAATACAAGAGGTTCCACAAGGACCAATGTGCGATCTACTCTGGTCTGATCC 7 AspAspArgCysGlyTrpGlyIleSerProArgGyAlaGlyTyThrPheGlyGlnAsp 2 [	281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300 ::::::	AF107464  AF107464  ON Hevea brasiliensis serine/threonine protein phosphatase type 2A (PP2A) mRNA, complete cds.  AF107464  N AF107464.1 GI:3986749  Hevea brasiliensis SM Hevea brasiliensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicocyledons; rossids; eurosids; lamparyadons; imalpighiales; Euphorbiaceae; Crotonoideae;	1 (bases 1 to 1370) Shin, D.H. and Han, KH. Isolation of a cDNA encoding a type 2A serine/threonine phosphatase (PCR9) (PCR99-011) Plant Physiol. 119, 364 (1999) 2 (bases 1 to 1370) Shin, D.H. and Han, KH. Direct Submission Submitted (17-NOV-1988) Kumho Life and Ruvironmental Sciaumitted (17-NOV-1988)	Laborator S urce ne	/product="serine/threonine protein phosphatase type 2A" /product="serine/threonine protein phosphatase type 2A" /protein id="AAD09953.1" /db_xref="G1:3986750" /db_xref="G1:3986750" /db_xref="G1:3986750" /db_xref="d1:3986750" /db_xref="d1:3986750" /db_xref="G1:3986

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FAIS Genome Sequencing & Analysis Group: Otomo,Y., I. Fujamura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobk Kodama,T., Ikeda,R., Ishibiki,J., Kawamata,M., Mobik Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H Mizuno,K., Nairikawa,R., Nikuta,J., Oka,M., Kyu,R., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Scand Genome Exploration Research Group in Riken Genomic Scand Genome Science Laboratory in Riken, Adachi,J., A. Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanag Hara,A., Hashizume,W., Hayashida,K., Hayatahi,N., Hiri Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K. Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kolima,Y., Kodo,S., X., Katoh,H., Kawai,J., Konno,H.	Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, P. Ota, Y., Saltoh, H., Sakai, C., Sakai, R., Sakaime, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shirak. Sagabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Ti Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Wal Yasunishi, A. and Hayashizaki, Y. Location/Qualifiers 1. 1563   Organism="Cryta sativa (japonica cultivar-index"   //mol Lype="mRNA"   /	t Similarity: 96.09% ocal Similarity: 96.09% Match: 150.33% 764-259-13 (1-306) x AK072676 (1- 1 Met ProSerTyrAlaAspValA 1 Met ProSerTyrAlaAspValA 1	Db 274 TGGAACGTGGCGGTGCCCGTCACHICHCHILLININININININININININININININININININ
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RESULT 13 RESULT 13 AK0726-6 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL PUBMED REFERNCE AUTHORS	TITLE JOURNAL COMMENT

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Saski,T., Kusumegi,T., Lu,M., Masuda,H
ikawa,R., Niikura,J., Oka,M., Ryu,R.,
Isuuki,Y., Tsunoda,Y., Ueda,M., Xie,Q.,
Matsubara,K. and Murakami,K.
tion Research Group in Riken Genomic Sc
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akawa,T., Carninci,P., Fukuda,S., Hana;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa
                                                                                                                                              Met ProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCy
                                                                                                                                                                      21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVa
                                                                                                                                                                                                                                                               61 GGTGAAGCAGACGTGAAGATCCTTTGCGATCAAGCTAAAGCGATTCTTGT
                                                                                                                                                                                                                                                                                                              AsnValGInProValLysCysProValThrValCysGlyAspIleHisGl
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S Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
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Collection and Clustering of RAFL CDNAS (RAFL CDNA: 'RIKEN
Arabidopsis Full-Length CDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
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CATGGGLSFSLDVLDNRRSLDRIQEVPHEGPMCDLLWSDPDORCGWGISPRGAGYTFG
QDIATOFNHNNGLSILSRAHQLVMEGYNWCGEKNVYTVFSAPNYCYRCGNMAAILEIG
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Location/Qualifiers
Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Cheuk, R., Hayashitzaki, Y., Tshida, J., Cheuk, R., Hayashitzaki, Y., Tshida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lan, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J. Sakurai, T., Satcu, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R. W., Ecker, J.R. and Theologis, A. Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G. Bowser,L., Chen,H., Meuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
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